



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Inouye, Sumiko
Hsu, Mei-Yin
Eagle, Susan
Inouye, Masayori

(ii) TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE

(iii) NUMBER OF SEQUENCES: 52

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/808,031
(B) FILING DATE: 03-MAR-1997
(C) CLASSIFICATION:

61 (viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 377(913).5888P

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 640..2094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCATCCGCGC GGACACCCCC TCCTACGTGC CCCCCGACGC GGAGAGCGGC GTGGAGACGG	60
TGTACCGCGT TTCCCTGGAT GGTCACCTGG TGGCGGTGGA GTGGGGCCCG CGCACGGGCT	120
CGCCGCGTCA CCAGCGGCTC TGGTTCGACT CGGATGCGGA AGCCCCCGGA GCCTACTTCG	180
CGCGCCTCGA GAAGTTGGCG GCTGACGGCT ACATCGACGC GGCCTCGGCA TTGGTCTAAA	240
CCCTTCAACC ACGGCTCGGC CGCCACGCGC GGCCGGCAGG ACAGGTGCGA CGAACAGACG	300
ACGACGTGCG CTTACGCGC GAGCAGCCGA GAGAGGTCCG GAGTGCATCA GCCTGAGCGC	360
CTCGAGCGGC GGAGCGGCGT TGCGCCGCTC CGGTTGGAAT GCAGGACACT CTCCGCAAGG	420
TAGCCTGTTC TTGGCTCTCT CCCTCCTAGG CACTACGGCC AGGGTGGGTA GCGGAGCCAA	480
CGACGCCACC GCCGTTTACC CACCCCGGCC GTAGTGCCTA GGAGGGGAGA GCCGGTGAGG	540
CTACCGTGCC CCAGGTAAGA TGGTGGTGCT TTCCCGGCCT CCGTCGACTG CTCGCGCCAT	600
GTCCCGTCTT CCATCGCCGC GCCCGCCCAA GGTGCAGAC ATG ACC GCC AGG CTG	654
Met Thr Ala Arg Leu	
1 5	
GAC CCG TTC GTC CCC GCA GCT TCG CCG CAG GCC GTG CCC ACG CCC GAG	702
Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala Val Pro Thr Pro Glu	
10 15 20	
CTC ACC GCT CCG TCG TCA GAC GCG GCC GCG AAG CGT GAA GCC CGC CGG	750
Leu Thr Ala Pro Ser Ser Asp Ala Ala Lys Arg Glu Ala Arg Arg	
25 30 35	
CTC GCG CAC GAA GCG TTG CTC GTC CGC GCG AAG GCC ATC GAC GAA GCG	798
Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala Ile Asp Glu Ala	
40 45 50	
GGC GGC GCC GAC GAC TGG GTG CAG GCG CAG CTC GTC TCC AAG GGG CTC	846
Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val Ser Lys Gly Leu	
55 60 65	
GCG GTC GAG GAC CTG GAC TTC TCC AGC GCC TCC GAG AAG GAC AAG AAG	894
Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu Lys Asp Lys Lys	
70 75 80 85	
GCC TGG AAG GAG AAG AAG AAG GCC GAG GCC ACC GAG CGC CGC GCG CTG	942
Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Leu	
90 95 100	
AAG CGT CAG GCG CAC GAG GCG TGG AAG GCC ACG CAC GTG GGC CAC CTG	990
Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His Val Gly His Leu	
105 110 115	
GGC GCG GGC GTG CAC TGG GCG GAG GAC CGC CTG GCC GAC GCG TTC GAC	1038
Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu Ala Asp Ala Phe Asp	
120 125 130	
GTG CCC CAC CGC GAG GAG CGC GCC CGG GCC AAC GGC CTG ACG GAG CTG	1086
Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn Gly Leu Thr Glu Leu	
135 140 145	

GAC Asp 150	TCC Ser	GCG Ala	GAG Glu	GCG Ala	CTG Leu	GCC Ala	AAG Lys	GCG Ala	CTG Leu	GGG Gly	CTG Leu	AGC Ser	GTC Val	TCC Ser	AAG Lys 165	1134
CTC Leu	CGC Arg	TGG Trp	TTC Phe	GCG Ala	TTC Phe	CAC His	CGG Arg	GAG Glu	GTC Val	GAC Asp	ACG Thr	GCC Ala	ACG Thr	CAC His	TAC Tyr 180	1182
GTG Val	AGC Ser	TGG Trp	ACC Thr	ATT Ile	CCG Pro	AAG Lys	CGG Arg	GAC Asp	GGC Gly	AGC Ser	AAG Lys	CGC Arg	ACG Thr	ATT Ile	ACG Thr 195	1230
TCC Ser	CCC Pro	AAG Lys	CCT Pro	GAG Glu	CTG Leu	AAG Lys	GCA Ala	GCG Ala	CAG Gln	CGC Arg	TGG Trp	GTG Val	CTG Leu	TCC Ser	AAC Asn 210	1278
GTC Val	GTG Val	GAG Glu	CGG Arg	CTG Leu	CCG Pro	GTC Val	CAC His	GGC Gly	GCC Ala	GCC Ala	CAC His	GGC Gly	TTC Phe	GTG Val	GCG Ala 225	1326
GGA Gly 230	CGC Arg	TCC Ser	ATC Ile	CTC Leu	ACC Thr	AAC Asn	GCG Ala	CTG Leu	GCC Ala	CAC His	CAG Gln	GGC Gly	GCG Ala	GAC Asp	GTC Val 245	1374
GTG Val	GTC Val	AAG Lys	GTG Val	GAC Asp	CTC Leu	AAG Lys	GAC Asp	TTC Phe	TTC Phe	CCC Pro	TCC Ser	GTC Val	ACC Thr	TGG Trp	CGC Arg 260	1422
CGG Arg	GTG Val	AAG Lys	GGC Gly	CTG Leu	TTG Leu	CGC Arg	AAG Lys	GGC Gly	GGC Gly	CTG Leu	CGG Arg	GAG Glu	GGC Gly	ACG Thr	TCC Ser 275	1470
ACG Thr	CTG Leu	CTG Leu	TCC Ser	CTC Leu	CTC Leu	TCC Ser	ACG Thr	GAA Glu	GCG Ala	CCG Pro	CGG Arg	GAG Glu	GCG Ala	GTC Val	CAG Gln 290	1518
TTC Phe	CGC Arg	GGC Gly	AAG Lys	CTC Leu	CTG Leu	CAC His	GTC Val	GCC Ala	AAG Lys	GGC Gly	CCG Pro	CGC Arg	GCC Ala	CTG Leu	CCC Pro 305	1566
CAG Gln 310	GGC Gly	GCC Ala	CCC Pro	ACG Thr	TCG Ser	CCC Pro	GGC Gly	ATC Ile	ACC Thr	AAC Asn	GCG Ala	CTC Leu	TGC Cys	CTG Leu	AAG Lys 325	1614
CTC Leu	GAC Asp	AAG Lys	CGG Arg	CTG Leu	TCC Ser	GCC Ala	CTC Leu	GCG Ala	AAG Lys	CGG Arg	CTG Leu	GGC Gly	TTC Phe	ACC Thr	TAC Tyr 340	1662
ACG Thr	CGC Arg	TAC Tyr	GCG Ala	GAC Asp	GAC Asp	CTG Leu	ACC Thr	TTC Phe	TCC Ser	TGG Trp	ACG Thr	AAG Lys	GCG Ala	AAG Lys	CAG Gln 355	1710
CCC Pro	AAG Lys	CCG Pro	CGG Arg	CGG Arg	ACG Thr	CAG Gln	CGT Arg	CCC Pro	CCC Pro	GTC Val	GCG Ala	GTC Val	CTC Leu	CTG Leu	TCT Ser 370	1758
CGC Arg	GTC Val	CAG Gln	GAA Glu	GTG Val	GTG Val	GAG Glu	GCG Ala	GAG Glu	GGC Gly	TTC Phe	CGC Arg	GTG Val	CAC His	CCG Pro	GAC Asp 385	1806

AAG ACG CGC GTC GCC CGC AAG GGC ACG CGG CAG CGG GTC ACC GGG CTC	1854
Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu	
390 395 400 405	
GTC GTG AAT GCG GCG GGC AAG GAC GCG CCC GCG GCC CGA GTC CCG CGC	1902
Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg	
410 415 420	
GAC GTC GTC CGC CAG CTC CGC GCC GCC ATC CAC AAC CGG AAG AAG GGC	1950
Asp Val Val Arg Gln Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly	
425 430 435	
AAG CCG GGC CGC GAG GGC GAG TCG CTC GAG CAG CTC AAG GGC ATG GCC	1998
Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala	
440 445 450	
GCC TTC ATC CAC ATG ACG GAC CCG GCC AAG GGC CGC GCC TTC CTG GCT	2046
Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala	
455 460 465	
CAG CTC ACG GAG CTC GAG TCC ACG GCG AGC GCC GCT CCG CAG GCG GAG	2094
Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu	
470 475 480 485	
TGACGCTCAG CGCGCGTCCG TCGCCGACGT GCCGCGCGCC AGCAACGCCG CATTAGCAA	2154
CTCCGTCAGC CGGCGCGGGT AC	2176

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Ala Arg Leu Asp Pro Phe Val Pro Ala Ala Ser Pro Gln Ala	
1 5 10 15	
Val Pro Thr Pro Glu Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys	
20 25 30	
Arg Glu Ala Arg Arg Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys	
35 40 45	
Ala Ile Asp Glu Ala Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu	
50 55 60	
Val Ser Lys Gly Leu Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser	
65 70 75 80	
Glu Lys Asp Lys Lys Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr	
85 90 95	
Glu Arg Arg Ala Leu Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr	
100 105 110	

His Val Gly His Leu Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu
 115 120 125
 Ala Asp Ala Phe Asp Val Pro His Arg Glu Glu Arg Ala Arg Ala Asn
 130 135 140
 Gly Leu Thr Glu Leu Asp Ser Ala Glu Ala Leu Ala Lys Ala Leu Gly
 145 150 155 160
 Leu Ser Val Ser Lys Leu Arg Trp Phe Ala Phe His Arg Glu Val Asp
 165 170 175
 Thr Ala Thr His Tyr Val Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser
 180 185 190
 Lys Arg Thr Ile Thr Ser Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg
 195 200 205
 Trp Val Leu Ser Asn Val Val Glu Arg Leu Pro Val His Gly Ala Ala
 210 215 220
 His Gly Phe Val Ala Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His
 225 230 235 240
 Gln Gly Ala Asp Val Val Val Lys Val Asp Leu Lys Asp Phe Phe Pro
 245 250 255
 Ser Val Thr Trp Arg Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu
 260 265 270
 Arg Glu Gly Thr Ser Thr Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro
 275 280 285
 Arg Glu Ala Val Gln Phe Arg Gly Lys Leu Leu His Val Ala Lys Gly
 290 295 300
 Pro Arg Ala Leu Pro Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn
 305 310 315 320
 Ala Leu Cys Leu Lys Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg
 325 330 335
 Leu Gly Phe Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp
 340 345 350
 Thr Lys Ala Lys Gln Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro Val
 355 360 365
 Ala Val Leu Leu Ser Arg Val Gln Glu Val Val Glu Ala Glu Gly Phe
 370 375 380
 Arg Val His Pro Asp Lys Thr Arg Val Ala Arg Lys Gly Thr Arg Gln
 385 390 395 400
 Arg Val Thr Gly Leu Val Val Asn Ala Ala Gly Lys Asp Ala Pro Ala
 405 410 415
 Ala Arg Val Pro Arg Asp Val Val Arg Gln Leu Arg Ala Ala Ile His
 420 425 430

Asn Arg Lys Lys Gly Lys Pro Gly Arg Glu Gly Glu Ser Leu Glu Gln
 435 440 445
 Leu Lys Gly Met Ala Ala Phe Ile His Met Thr Asp Pro Ala Lys Gly
 450 455 460
 Arg Ala Phe Leu Ala Gln Leu Thr Glu Leu Glu Ser Thr Ala Ser Ala
 465 470 475 480
 Ala Pro Gln Ala Glu
 485

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro
 1 5 10 15
 Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met
 20 25 30
 Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn
 35 40 45
 Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys
 50 55 60
 Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu
 65 70 75 80
 Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser
 85 90 95
 Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp
 100 105 110
 Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn
 115 120 125
 Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp
 130 135 140
 Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu
 145 150 155 160
 Pro Phe Lys Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp
 165 170 175

Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys
 180 185 190
 Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro
 195 200 205
 Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu
 210 215 220
 Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys
 225 230 235 240
 Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn
 245 250 255
 Trp Ala Ser Gln Ile Tyr Pro
 260

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Pro Trp Ala Arg Thr Pro Pro Lys Ala Pro Arg Asn Gln Pro Val
 1 5 10 15
 Pro Phe Lys Pro Glu Arg Leu Gln Ala Leu Gln His Leu Val Arg Lys
 20 25 30
 Ala Leu Glu Ala Gly His Ile Glu Pro Tyr Thr Gly Pro Gly Asn Asn
 35 40 45
 Pro Val Phe Pro Val Lys Lys Ala Asn Gly Thr Trp Arg Phe Ile His
 50 55 60
 Asp Leu Arg Ala Thr Asn Ser Leu Thr Ile Asp Leu Ser Ser Ser Ser
 65 70 75 80
 Pro Gly Pro Pro Asp Leu Ser Ser Leu Pro Thr Thr Leu Ala His Leu
 85 90 95
 Gln Thr Ile Asp Leu Arg Asp Ala Phe Phe Gln Ile Pro Leu Pro Lys
 100 105 110
 Gln Phe Gln Pro Tyr Phe Ala Phe Thr Val Pro Gln Gln Cys Asn Tyr
 115 120 125
 Gly Pro Gly Thr Arg Tyr Ala Trp Lys Val Leu Pro Gln Gly Phe Lys
 130 135 140

Asn Ser Pro Thr Leu Phe Glu Met Gln Leu Ala His Ile Leu Gln Pro
 145 150 155 160
 Ile Arg Gln Ala Phe Pro Gln Cys Thr Ile Leu Gln Tyr Met Asp Asp
 165 170 175
 Ile Leu Leu Ala Ser Pro Ser His Glu Asp Leu Leu Leu Leu Ser Glu
 180 185 190
 Ala Thr Met Ala Ser Leu Ile Ser His Gly Leu Pro Val Ser Glu Asn
 195 200 205
 Lys Thr Gln Gln Thr Pro Gly Thr Ile Lys Phe Leu Gly Gln Ile Ile
 210 215 220
 Ser Pro Asn His Leu Thr Tyr Asp Ala Val Pro Thr Val Pro Ile Arg
 225 230 235 240
 Ser Arg Trp Ala Leu Pro Glu Leu Gln Ala Leu Leu Gly Glu Ile Gln
 245 250 255
 Trp Val Ser Lys Gly Thr Pro
 260

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr
 1 5 10 15
 Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp
 20 25 30
 Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys
 35 40 45
 Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe
 50 55 60
 Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg
 65 70 75 80
 Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser
 85 90 95
 Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe
 100 105 110

Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr
 115 120 125
 Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn
 130 135 140
 Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys
 145 150 155 160
 Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr
 165 170 175
 Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly
 180 185 190
 Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe
 195 200 205
 Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln
 210 215 220
 Glu Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys
 225 230 235 240
 Tyr Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly
 245 250 255
 Glu Tyr Lys

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr Val Ser Trp Thr
 1 5 10 15
 Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr Ser Pro Lys Pro
 20 25 30
 Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn Val Val Glu Arg
 35 40 45
 Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly Arg Ser Ile
 50 55 60
 Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val Val Lys Val
 65 70 75 80

Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg Arg Val Lys Gly
 85 90 95
 Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser Thr Leu Leu Ser
 100 105 110
 Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln Phe Arg Gly Lys
 115 120 125
 Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro Gln Gly Ala Pro
 130 135 140
 Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys Leu Asp Lys Arg
 145 150 155 160
 Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr Thr Arg Tyr Ala
 165 170 175
 Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln Pro Lys Pro Arg
 180 185 190
 Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser Arg Val Gln Glu
 195 200 205
 Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp Lys Thr Arg Val
 210 215 220
 Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu Val Val Asn Ala
 225 230 235 240
 Ala Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg Asp Val Val Arg
 245 250 255
 Gln Leu Arg Ala Ala Ile His Asn Arg Lys
 260 265

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 111 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Thr Pro Glu Leu Thr Ala Pro Ser Ser Asp Ala Ala Ala Lys Arg
 1 5 10 15
 Glu Ala Arg Arg Leu Ala His Glu Ala Leu Leu Val Arg Ala Lys Ala
 20 25 30
 Ile Asp Glu Ala Gly Gly Ala Asp Asp Trp Val Gln Ala Gln Leu Val
 35 40 45

Ser Lys Gly Leu Ala Val Glu Asp Leu Asp Phe Ser Ser Ala Ser Glu
50 55 60

Lys Asp Lys Lys Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu
65 70 75 80

Arg Arg Ala Leu Lys Arg Gln Ala His Glu Ala Trp Lys Ala Thr His
85 90 95

Val Gly His Leu Gly Ala Gly Val His Trp Ala Glu Asp Arg Leu
100 105 110

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Pro Asp Pro Asp Met Thr Arg Val Thr Asn Ser Pro Ser Leu Gln Ala
1 5 10 15

His Leu Gln Ala Leu Tyr Leu Val Gln His Glu Val Trp Arg Pro Leu
20 25 30

Ala Ala Ala Tyr Gln Glu Gln Leu Asp Arg Pro Val Val Pro His Pro
35 40 45

Tyr Arg Val Gly Asp Thr Val Trp Val Arg Arg His Gln Thr Lys Asn
50 55 60

Leu Glu Pro Arg Trp Lys Gly Pro Tyr Thr Val Leu Leu Thr Thr Pro
65 70 75 80

Thr Ala Leu Lys Val Asp Gly Ile Ala Ala Trp Ile His Ala Ala His
85 90 95

Val Lys Ala Ala Asp Pro Gly Gly Gly Pro Ser Ser Arg Leu
100 105 110

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Lys Asp Ala Pro Ala Ala Arg Val Pro Arg Asp Val Val Arg Gln
1 5 10 15
Leu Arg Ala Ala Ile His Asn Arg Lys Lys Gly Lys Pro Gly Arg Glu
20 25 30
Gly Glu Ser Leu Glu Gln Leu Lys Gly Met Ala Ala Phe Ile His Met
35 40 45
Thr Asp Pro Ala Lys Gly Arg Ala Phe Leu Ala Gln Leu Thr Glu Leu
50 55 60
Glu Ser Thr Ala Ser Ala Ala Pro Gln Ala Glu
65 70 75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Lys Glu Gly His Ser Ala Arg Gln Cys Arg Ala Pro Arg Arg Gln
1 5 10 15
Gly Cys Trp Lys Cys Gly Lys Pro Gly His Ile Met Thr Asn Cys Pro
20 25 30
Asp Arg Gln Ala Gly Phe Leu Gly Leu Gly Pro Trp Gly Lys Lys Pro
35 40 45
Arg Asn Phe Pro Val Ala Gln Val Pro Gln Gly Leu Thr Pro Thr Ala
50 55 60
Pro Pro
65

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Pro Arg Ala Leu Pro Gln Gly Ala Pro Thr Ser Pro Gly Ile Thr
1 5 10 15
Asn Ala Leu Cys Leu Lys Leu Asp Lys Arg Leu Ser Ala Leu Ala Lys
20 25 30
Arg Leu Gly Phe Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser
35 40 45
Trp Thr Lys Ala Lys Gln Pro Lys Pro Arg Arg Thr Gln Arg Pro Pro
50 55 60
Val Ala Val Leu
65

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Tyr Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser
1 5 10 15
Asn Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys
20 25 30
Lys Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser
35 40 45
Thr Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu
50 55 60
Gly Val Val Leu
65

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Tyr Lys Asn Leu Leu Pro Gln Gly Ala Pro Ser Ser Pro Lys Leu Ala
1 5 10 15
Asn Leu Ile Cys Ser Lys Leu Asp Tyr Arg Ile Gln Gly Tyr Ala Gly
20 25 30
Ser Arg Gly Leu Ile Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Leu Ser
35 40 45
Ala Gln Ser Met Lys Lys Val Val Lys Ala Arg Asp Phe Leu Phe Ser
50 55 60
Ile Ile Pro Ser
65

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile
1 5 10 15
Phe Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Lys Lys Gln Asn
20 25 30
Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser
35 40 45
Asp Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln
50 55 60
His Leu Leu
65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Tyr Ala Trp Lys Val Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu
1 5 10 15
Phe Glu Met Gln Leu Ala His Ile Leu Gln Pro Ile Arg Gln Ala Phe
20 25 30
Pro Gln Cys Thr Ile Leu Gln Tyr Met Asp Asp Ile Leu Leu Ala Ser
35 40 45
Pro Ser His Glu Asp Leu Leu Leu Leu Ser Glu Ala Thr Met Ala Ser
50 55 60
Leu Ile
65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Leu Thr Trp Thr Arg Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu
1 5 10 15
Phe Asp Glu Ala Leu His Arg Asp Leu Ala Asp Phe Arg Ile Gln His
20 25 30
Pro Asp Leu Ile Leu Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala
35 40 45
Thr Ser Glu Leu Asp Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe Gln Trp Lys Val Leu Pro Gln Gly Met Thr Cys Ser Pro Thr Ile
1 5 10 15
Cys Gln Leu Val Val Gly Gln Val Leu Glu Pro Leu Arg Leu Lys His
20 25 30
Pro Ser Leu Cys Met Leu His Tyr Met Asp Asp Leu Leu Leu Ala Ala
35 40 45
Ser Ser His Asp Gly Leu Glu Ala Ala Gly Glu Glu Val Ile Ser Thr
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Ala Trp Arg Val Leu Pro Gln Gly Phe Ile Asn Ser Pro Ala Leu
1 5 10 15
Phe Glu Arg Ala Leu Gln Glu Pro Leu Arg Gln Val Ser Ala Ala Phe
20 25 30
Ser Gln Ser Leu Leu Val Ser Tyr Met Asp Asp Ile Leu Tyr Ala Ser
35 40 45
Pro Thr Glu Glu Gln Arg Ser Gln Cys Tyr Gln Ala Leu Ala Ala Arg
50 55 60
Leu
65

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ile Ala Thr Asn Gly Val Pro Gln Gly Ala Ser Thr Ser Cys Gly Leu
1 5 10 15
Ala Thr Tyr Asn Val Leu Glu Leu Phe Leu Arg Tyr Asp Glu Leu Ile
20 25 30
Met Tyr Ala Asp Asp Gly Ile Leu Cys Arg Gln Asp Pro Ser Thr Pro
35 40 45
Asp Phe Ser Val Glu Glu Ala Gly Val Val Gln Glu Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr Glu Tyr Leu Arg Met Pro Phe Gly Leu Lys Asn Ala Pro Ala Thr
1 5 10 15
Phe Gln Arg Cys Met Asn Asp Ile Leu Arg Pro Leu Leu Asn Lys His
20 25 30
Cys Leu Val Tyr Leu Asp Asp Ile Ile Val Phe Ser Thr Ser Leu Asp
35 40 45
Glu His Leu Gln Ser Leu Gly Leu Val Phe Glu Lys Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Tyr Glu Phe Cys Arg Leu Pro Phe Gly Leu Arg Asn Ala Ser Ser Ile
1 5 10 15
Phe Gln Arg Ala Leu Asp Asp Val Leu Arg Glu Gln Ile Gly Lys Ile
20 25 30

Cys Tyr Val Tyr Val Asp Asp Val Ile Ile Phe Ser Glu Asn Glu Ser
 35 40 45
 Asp His Val Arg His Ile Asp Thr Val Leu Lys Cys Leu
 50 55 60

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Cys Lys Leu Asn Lys Ala Ile Tyr Gly Leu Lys Gln Ala Ala Arg Cys
 1 5 10 15
 Trp Phe Arg Cys Ile Tyr Ile Leu Asp Lys Gly Asn Ile Asn Glu Asn
 20 25 30
 Ile Tyr Val Leu Leu Tyr Val Asp Asp Val Val Ile Ala Thr Gly Asp
 35 40 45
 Met Thr Arg Met Asn Asn Phe Lys Arg Tyr Leu Met Glu Lys Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Cys Leu Leu Lys Lys Ser Leu Tyr Gly Leu Lys Gln Ser Pro Arg Gln
 1 5 10 15
 Trp Asn Ala Cys Val Tyr Val Lys Gln Val Ser Glu Gln Glu His Leu
 20 25 30
 Tyr Leu Leu Leu Tyr Val Asp Asp Met Leu Ile Ala Gly Lys Ser Lys
 35 40 45
 Ser Glu Ile Asn Lys Val Lys Glu Gln Leu Ser Met Glu Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Ile Arg Leu Lys Lys Ser Leu Tyr Glu Leu Lys Gln Ser Gly Ala Asn
1           5           10           15
Trp Tyr Glu Glu Val Arg Gly Trp Ser Cys Val Phe Lys Asn Ser Gln
          20           25           30
Val Thr Ile Cys Leu Phe Val Asp Asp Met Val Leu Phe Ser Lys Asn
          35           40           45
Leu Asn Ser Asn Lys Arg Ile Ile Glu Lys Leu Lys Met Gln Tyr
          50           55           60
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "The 2' position of this nucleotide is linked to the 5' position of nucleotide number one of SEQ ID NO:26 of this application."

(ix) FEATURE:

- (A) NAME/KEY: misc_binding
- (B) LOCATION: 52..58
- (D) OTHER INFORMATION: /product= "This region can hydrogen bond to nucleotides 61-67 of SEQ ID NO:26 of this application."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CACGCAUGUA GGCAGAUUUG UUGGUUGUGA AUCGCAACCA GUGGCCUUAU UGGCAGGA

58

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1
(D) OTHER INFORMATION: /product= "The 2' position of this nucleotide is linked to the 5' position of nucleotide number fifteen of SEQ ID NO:25 of this application."

(ix) FEATURE:
(A) NAME/KEY: misc_binding
(B) LOCATION: 61..67
(D) OTHER INFORMATION: /product= "This region can hydrogen bond to nucleotides 52-58 of SEQ ID NO:25 of this application."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
TCCTTCGCAC AGCACACCTG CCGTATAGCT CTGAATCAAG GATTTTAGGG AGGCGATTCC 60
TCCTGCC 67
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2423 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 418..2175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
TGGCCATTNA GATACGGATT TTCACTTCCT TGACAGTGCA TGACTATGCT GCATGAAATN 60
GCATGATCGA TTGAGGATCG TCTTTGCTCA GATCCGCCAG AACTGGCGGG CTTTGTCTCA 120
TGTCATGCAT GTGCATGAAA ACCACTGCAT AAAGCGGGCA GGCGTGGCGG GGATACGAGC 180
GCGCGCTATC ACCGAAAATA GCCAAAATAC TTCTGGAAAA CAGAAAGTTG AAGTGATATG 240
TTCATAAACA CGCATGTAGG CAGATTTGTT GGTGTGAAT CGCAACCAGT GGCCTTAATG 300
GCAGGAGGAA TCGCCTCCCT AAAATCCTTG ATTCAGAGCT ATACGGCAGG TGTGCTGTGC 360
GAAGGAGTGC CTGCATGCGT TTCTCCTTGG CCTTTTTTCC TCTGGGATGA AGAAGAA 417
ATG ACA AAA ACA TCT AAA CTT GAC GCA CTT AGG GCT GCT ACT TCA CGT 465
Met Thr Lys Thr Ser Lys Leu Asp Ala Leu Arg Ala Ala Thr Ser Arg
  1             5             10             15
```

GAA GAC TTG GCT AAA ATT TTA GAT ATT AAG TTG GTA TTT TTA ACT AAC Glu Asp Leu Ala Lys Ile Leu Asp Ile Lys Leu Val Phe Leu Thr Asn 20 25 30	513
GTT CTA TAT AGA ATC GGC TCG GAT AAT CAA TAC ACT CAA TTT ACA ATA Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr Ile 35 40 45	561
CCG AAG AAA GGA AAA GGG GTA AGG ACT ATT TCT GCA CCT ACA GAC CGG Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp Arg 50 55 60	609
TTG AAG GAC ATC CAA CGA AGA ATA TGT GAC TTA CTT TCT GAT TGT AGA Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys Arg 65 70 75 80	657
GAT GAG ATC TTT GCT ATA AGG AAA ATT AGT AAC AAC TAT TCC TTT GGT Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe Gly 85 90 95	705
TTT GAG AGG GGA AAA TCA ATA ATC CTA AAT GCT TAT AAG CAT AGA GGC Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg Gly 100 105 110	753
AAA CAA ATA ATA TTA AAT ATA GAT CTT AAG GAT TTT TTT GAA AGC TTT Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser Phe 115 120 125	801
AAT TTT GGA CGA GTT AGA GGA TAT TTT CTT TCC AAT CAG GAT TTT TTA Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe Leu 130 135 140	849
TTA AAT CCT GTG GTG GCA ACG ACA CTT GCA AAA GCT GCA TGC TAT AAT Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr Asn 145 150 155 160	897
GGA ACC CTC CCC CAA GGA AGT CCA TGT TCT CCT ATT ATC TCA AAT CTA Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn Leu 165 170 175	945
ATT TGC AAT ATT ATG GAT ATG AGA TTA GCT AAG CTG GCT AAA AAA TAT Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys Tyr 180 185 190	993
GGA TGT ACT TAT AGC AGA TAT GCT GAT GAT ATA ACA ATT TCT ACA AAT Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr Asn 195 200 205	1041
AAA AAT ACA TTT CCG TTA GAA ATG GCT ACT GTG CAA CCT GAA GGG GTT Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly Val 210 215 220	1089
GTT TTG GGA AAA GTT TTG GTA AAA GAA ATA GAA AAC TCT GGA TTC GAA Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe Glu 225 230 235 240	1137
ATA AAT GAT TCA AAG ACT AGG CTT ACG TAT AAG ACA TCA AGG CAA GAA Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln Glu 245 250 255	1185

GTA ACG GGA CTT ACA GTT AAC AGA ATC GTT AAT ATT GAT AGA TGT TAT Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys Tyr 260 265 270	1233
TAT AAA AAA ACT CGG GCG TTG GCA CAT GCT TTG TAT CGT ACA GGT GAA Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly Glu 275 280 285	1281
TAT AAA GTG CCA GAT GAA AAT GGT GTT TTA GTT TCA GGA GGT CTG GAT Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu Asp 290 295 300	1329
AAA CTT GAG GGG ATG TTT GGT TTT ATT GAT CAA GTT GAT AAG TTT AAC Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe Asn 305 310 315 320	1377
AAT ATA AAG AAA AAA CTG AAC AAG CAA CCT GAT AGA TAT GTA TTG ACT Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu Thr 325 330 335	1425
AAT GCG ACT TTG CAT GGT TTT AAA TTA AAG TTG AAT GCG CGA GAA AAA Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu Lys 340 345 350	1473
GCA TAT AGT AAA TTT ATT TAC TAT AAA TTT TTT CAT GGC AAC ACC TGT Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr Cys 355 360 365	1521
CCT ACG ATA ATT ACA GAA GGG AAG ACT GAT CGG ATA TAT TTG AAG GCT Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys Ala 370 375 380	1569
GCT TTG CAT TCT TTG GAG ACA TCA TAT CCT GAG TTG TTT AGA GAA AAA Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu Lys 385 390 395 400	1617
ACA GAT AGT AAA AAG AAA GAA ATA AAT CTT AAT ATA TTT AAA TCT AAT Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser Asn 405 410 415	1665
GAA AAG ACC AAA TAT TTT TTA GAT CTT TCT GGG GGA ACT GCA GAT CTG Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp Leu 420 425 430	1713
AAA AAA TTT GTA GAG CGT TAT AAA AAT AAT TAT GCT TCT TAT TAT GGT Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr Gly 435 440 445	1761
TCT GTT CCA AAA CAG CCA GTG ATT ATG GTT CTT GAT AAT GAT ACA GGT Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr Gly 450 455 460	1809
CCA AGC GAT TTA CTT AAT TTT CTG CGC AAT AAA GTT AAA AGC TGC CCA Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys Pro 465 470 475 480	1857
GAC GAT GTA ACT GAA ATG AGA AAG ATG AAA TAT ATT CAT GTT TTC TAT Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe Tyr 485 490 495	1905

AAT TTA TAT ATA GTT CTC ACA CCA TTG AGT CCT TCC GGC GAA CAA ACT Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln Thr 500 505 510	1953
TCA ATG GAG GAT CTT TTC CCT AAA GAT ATT TTA GAT ATC AAG ATT GAT Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile Asp 515 520 525	2001
GGT AAG AAA TTC AAC AAA AAT AAT GAT GGA GAC TCA AAA ACG GAA TAT Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu Tyr 530 535 540	2049
GGG AAG CAT ATT TTT TCC ATG AGG GTT GTT AGA GAT AAA AAG CGG AAA Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg Lys 545 550 555 560	2097
ATA GAT TTT AAG GCA TTT TGT TGT ATT TTT GAT GCT ATA AAA GAT ATA Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp Ile 565 570 575	2145
AAG GAA CAT TAT AAA TTA ATG TTA AAT AGC TAATGAACAG CCCTAACGTT Lys Glu His Tyr Lys Leu Met Leu Asn Ser 580 585	2195
ATGAACGCTA AGGCTGATTT TTCGTTAAAA TTTATATGGT TTGAATTGTA ATATATTATC	2255
TTCAAGCCAT TTATTTAATT CCTGCATCCT TTTCTGTAAG GGTATTAATT CGTTCCTCAC	2315
AAACACTAAA CTCGCTTTTT CCACATCCCC AAACCCCCCT AACATTATTC GGCATAATCC	2375
CCATCATTTG CGGTGGCACA CGATGCGCTG CCATCATGTC ATCGCGGC	2423

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 586 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Thr Lys Thr Ser Lys Leu Asp Ala Leu Arg Ala Ala Thr Ser Arg 1 5 10 15
Glu Asp Leu Ala Lys Ile Leu Asp Ile Lys Leu Val Phe Leu Thr Asn 20 25 30
Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr Ile 35 40 45
Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp Arg 50 55 60
Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys Arg 65 70 75 80
Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe Gly 85 90 95

Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg Gly
 100 105 110
 Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser Phe
 115 120 125
 Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe Leu
 130 135 140
 Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr Asn
 145 150 155 160
 Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn Leu
 165 170 175
 Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys Tyr
 180 185 190
 Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr Asn
 195 200 205
 Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly Val
 210 215 220
 Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe Glu
 225 230 235 240
 Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln Glu
 245 250 255
 Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys Tyr
 260 265 270
 Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly Glu
 275 280 285
 Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu Asp
 290 295 300
 Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe Asn
 305 310 315 320
 Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu Thr
 325 330 335
 Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu Lys
 340 345 350
 Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr Cys
 355 360 365
 Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys Ala
 370 375 380
 Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu Lys
 385 390 395 400
 Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser Asn
 405 410 415

Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp Leu
420 425 430

Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr Gly
435 440 445

Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr Gly
450 455 460

Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys Pro
465 470 475 480

Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe Tyr
485 490 495

Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln Thr
500 505 510

Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile Asp
515 520 525

Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu Tyr
530 535 540

Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg Lys
545 550 555 560

Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp Ile
565 570 575

Lys Glu His Tyr Lys Leu Met Leu Asn Ser
580 585

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val Lys Gln Trp Pro
1 5 10 15

Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys Thr Glu Met
20 25 30

Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn Pro Tyr Asn
35 40 45

Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys Trp Arg Lys
50 55 60

Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu
 65 70 75 80
 Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys Lys Lys Ser
 85 90 95
 Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp
 100 105 110
 Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn
 115 120 125
 Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp
 130 135 140
 Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys Ile Leu Glu
 145 150 155 160
 Pro Phe Lys Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp
 165 170 175
 Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His Arg Thr Lys
 180 185 190
 Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu Thr Thr Pro
 195 200 205
 Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu
 210 215 220
 Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu Pro Glu Lys
 225 230 235 240
 Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly Lys Leu Asn
 245 250 255
 Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln Leu Cys Lys
 260 265 270
 Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro Leu Thr Glu
 275 280 285
 Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro
 290 295 300
 Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile
 305 310 315 320
 Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro
 325 330 335
 Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met Arg Gly Ala His
 340 345 350
 Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln Lys Ile Thr Thr
 355 360 365
 Glu Ser Ile Val Ile Trp Gly Lys Thr Pro Lys Phe Lys Leu Pro Ile
 370 375 380

Gln Lys Glu Thr Trp Glu Thr Trp Trp Thr Glu Tyr Trp Gln Ala Thr
 385 390 395 400
 Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro Leu Val Lys Leu
 405 410 415
 Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala Glu Thr Phe Tyr
 420 425 430
 Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly Lys Ala Gly Tyr
 435 440 445
 Val Thr Asn Lys Gly Arg Gln Lys Val Val Pro Leu Thr Asn Thr Thr
 450 455 460
 Asn Gln Lys Thr Glu Leu Gln Ala Ile Tyr Leu Ala Leu Gln Asp Ser
 465 470 475 480
 Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr Ala Leu Gln Ile
 485 490 495
 Ile Gln Ala Gln Pro Asp Lys Ser Glu Ser Glu Leu Val Asn Gln Ile
 500 505 510
 Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu Ala Trp Val Pro
 515 520 525
 Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp Lys Leu Val Ser
 530 535 540
 Ala Gly
 545

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 578 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Arg Pro Trp Ala Arg Thr Pro Pro Lys Ala Pro Arg Asn Gln Pro Val
 1 5 10 15
 Pro Phe Lys Pro Glu Arg Leu Gln Ala Leu Gln His Leu Val Arg Lys
 20 25 30
 Ala Leu Glu Ala Gly His Ile Glu Pro Tyr Thr Gly Pro Gly Asn Asn
 35 40 45
 Pro Val Phe Pro Val Lys Lys Ala Asn Gly Thr Trp Arg Phe Ile His
 50 55 60

Asp Leu Arg Ala Thr Asn Ser Leu Thr Ile Asp Leu Ser Ser Ser Ser
 65 70 75 80
 Pro Gly Pro Pro Asp Leu Ser Ser Leu Pro Thr Thr Leu Ala His Leu
 85 90 95
 Gln Thr Ile Asp Leu Arg Asp Ala Phe Phe Gln Ile Pro Leu Pro Lys
 100 105 110
 Gln Phe Gln Pro Tyr Phe Ala Phe Thr Val Pro Gln Gln Cys Asn Tyr
 115 120 125
 Gly Pro Gly Thr Arg Tyr Ala Trp Lys Val Leu Pro Gln Gly Phe Lys
 130 135 140
 Asn Ser Pro Thr Leu Phe Glu Met Gln Leu Ala His Ile Leu Gln Pro
 145 150 155 160
 Ile Arg Gln Ala Phe Pro Gln Cys Thr Ile Leu Gln Tyr Met Asp Asp
 165 170 175
 Ile Leu Leu Ala Ser Pro Ser His Glu Asp Leu Leu Leu Leu Ser Glu
 180 185 190
 Ala Thr Met Ala Ser Leu Ile Ser His Gly Leu Pro Val Ser Glu Asn
 195 200 205
 Lys Thr Gln Gln Thr Pro Gly Thr Ile Lys Phe Leu Gly Gln Ile Ile
 210 215 220
 Ser Pro Asn His Leu Thr Tyr Asp Ala Val Pro Thr Val Pro Ile Arg
 225 230 235 240
 Ser Arg Trp Ala Leu Pro Glu Leu Gln Ala Leu Leu Gly Glu Ile Gln
 245 250 255
 Trp Val Ser Lys Gly Thr Pro Thr Leu Arg Gln Pro Leu His Ser Leu
 260 265 270
 Tyr Cys Ala Leu Gln Arg His Thr Asp Pro Arg Asp Gln Ile Tyr Leu
 275 280 285
 Asn Pro Ser Gln Val Gln Ser Leu Val Gln Leu Arg Gln Ala Leu Ser
 290 295 300
 Gln Asn Cys Arg Ser Arg Leu Val Gln Thr Leu Pro Leu Leu Gly Ala
 305 310 315 320
 Ile Met Leu Thr Leu Thr Gly Thr Thr Thr Val Val Phe Gln Ser Lys
 325 330 335
 Glu Gln Trp Pro Leu Val Trp Leu His Ala Pro Leu Pro His Thr Ser
 340 345 350
 Gln Cys Pro Trp Gly Gln Leu Leu Ala Ser Ala Val Leu Leu Leu Asp
 355 360 365
 Lys Tyr Thr Leu Gln Ser Tyr Gly Leu Leu Cys Gln Thr Ile His His
 370 375 380

Asn Ile Ser Thr Gln Thr Phe Asn Gln Phe Ile Gln Thr Ser Asp His
 385 390 395 400
 Pro Ser Val Pro Ile Leu Leu His His Ser His Arg Phe Lys Asn Leu
 405 410 415
 Gly Ala Gln Thr Gly Glu Leu Trp Asn Thr Phe Leu Lys Thr Ala Ala
 420 425 430
 Pro Leu Ala Pro Val Lys Ala Leu Met Pro Val Phe Thr Leu Ser Pro
 435 440 445
 Val Ile Ile Asn Thr Ala Pro Cys Leu Phe Ser Asp Gly Ser Thr Ser
 450 455 460
 Arg Ala Ala Tyr Ile Leu Trp Asp Lys Gln Ile Leu Ser Gln Arg Ser
 465 470 475 480
 Phe Pro Leu Pro Pro Pro His Lys Ser Ala Gln Arg Ala Glu Leu Leu
 485 490 495
 Gly Leu Leu His Gly Leu Ser Ser Ala Arg Ser Trp Arg Cys Leu Asn
 500 505 510
 Ile Phe Leu Asp Ser Lys Tyr Leu Tyr His Tyr Leu Arg Thr Leu Ala
 515 520 525
 Leu Gly Thr Phe Gln Gly Arg Ser Ser Gln Ala Pro Phe Gln Ala Leu
 530 535 540
 Leu Pro Arg Leu Leu Ser Arg Lys Val Val Tyr Leu His His Val Arg
 545 550 555 560
 Ser His Thr Asn Leu Pro Asp Pro Ile Ser Arg Leu Asn Ala Leu Thr
 565 570 575
 Asp Ala

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr Gln Phe Thr
 1 5 10 15
 Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala Pro Thr Asp
 20 25 30

Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu Ser Asp Cys
 35 40 45
 Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn Tyr Ser Phe
 50 55 60
 Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr Lys His Arg
 65 70 75 80
 Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe Phe Glu Ser
 85 90 95
 Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn Gln Asp Phe
 100 105 110
 Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala Ala Cys Tyr
 115 120 125
 Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile Ile Ser Asn
 130 135 140
 Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu Ala Lys Lys
 145 150 155 160
 Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr Ile Ser Thr
 165 170 175
 Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln Pro Glu Gly
 180 185 190
 Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn Ser Gly Phe
 195 200 205
 Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr Ser Arg Gln
 210 215 220
 Glu Val Thr Gly Leu Thr Val Asn Arg Ile Val Asn Ile Asp Arg Cys
 225 230 235 240
 Tyr Tyr Lys Lys Thr Arg Ala Leu Ala His Ala Leu Tyr Arg Thr Gly
 245 250 255
 Glu Tyr Lys Val Pro Asp Glu Asn Gly Val Leu Val Ser Gly Gly Leu
 260 265 270
 Asp Lys Leu Glu Gly Met Phe Gly Phe Ile Asp Gln Val Asp Lys Phe
 275 280 285
 Asn Asn Ile Lys Lys Lys Leu Asn Lys Gln Pro Asp Arg Tyr Val Leu
 290 295 300
 Thr Asn Ala Thr Leu His Gly Phe Lys Leu Lys Leu Asn Ala Arg Glu
 305 310 315 320
 Lys Ala Tyr Ser Lys Phe Ile Tyr Tyr Lys Phe Phe His Gly Asn Thr
 325 330 335
 Cys Pro Thr Ile Ile Thr Glu Gly Lys Thr Asp Arg Ile Tyr Leu Lys
 340 345 350

Ala Ala Leu His Ser Leu Glu Thr Ser Tyr Pro Glu Leu Phe Arg Glu
355 360 365

Lys Thr Asp Ser Lys Lys Lys Glu Ile Asn Leu Asn Ile Phe Lys Ser
370 375 380

Asn Glu Lys Thr Lys Tyr Phe Leu Asp Leu Ser Gly Gly Thr Ala Asp
385 390 395 400

Leu Lys Lys Phe Val Glu Arg Tyr Lys Asn Asn Tyr Ala Ser Tyr Tyr
405 410 415

Gly Ser Val Pro Lys Gln Pro Val Ile Met Val Leu Asp Asn Asp Thr
420 425 430

Gly Pro Ser Asp Leu Leu Asn Phe Leu Arg Asn Lys Val Lys Ser Cys
435 440 445

Pro Asp Asp Val Thr Glu Met Arg Lys Met Lys Tyr Ile His Val Phe
450 455 460

Tyr Asn Leu Tyr Ile Val Leu Thr Pro Leu Ser Pro Ser Gly Glu Gln
465 470 475 480

Thr Ser Met Glu Asp Leu Phe Pro Lys Asp Ile Leu Asp Ile Lys Ile
485 490 495

Asp Gly Lys Lys Phe Asn Lys Asn Asn Asp Gly Asp Ser Lys Thr Glu
500 505 510

Tyr Gly Lys His Ile Phe Ser Met Arg Val Val Arg Asp Lys Lys Arg
515 520 525

Lys Ile Asp Phe Lys Ala Phe Cys Cys Ile Phe Asp Ala Ile Lys Asp
530 535 540

Ile Lys Glu His Tyr Lys Leu Met Leu Asn Ser
545 550 555

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Arg Trp Phe Ser Phe His Arg Glu Val Asp Thr Gly Thr His Tyr Gln
1 5 10 15

Thr Trp Glu Ile Pro Lys Arg Asp Gly Gly Lys Arg Thr Leu Thr Ala
20 25 30

Pro Lys Arg Glu Leu Lys Ala Val Gln Arg Trp Val Leu Ala Asn Val
 35 40 45
 Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly
 50 55 60
 Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val
 65 70 75 80
 Val Lys Val Asp Met Lys Asp Phe Phe Pro Ser Val Thr Trp Pro Arg
 85 90 95
 Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Pro Glu Asn Leu Ala Thr
 100 105 110
 Leu Leu Ala Leu Leu Ser Thr Glu Ala Pro Arg Glu Val Val Arg Phe
 115 120 125
 Arg Gly Glu Thr Leu Tyr Val Ala Lys Gly Ala Arg Ala Leu Pro Gln
 130 135 140
 Gly Ala Pro Thr Ser Pro Ala Leu Thr Asn Ala Leu Cys Leu Arg Leu
 145 150 155 160
 Asp Lys Arg Leu Ser Ala Leu Ser Lys Arg Leu Gly Phe Thr Tyr Thr
 165 170 175
 Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Arg Arg Ala Lys Lys Ser
 180 185 190
 Arg Gln Lys Glu Leu Pro Leu Ala Asp Ala Pro Val Ala Leu Leu Leu
 195 200 205
 Ala Arg Val Lys Gly Val Leu Glu Ala Glu Gly Phe Thr Leu His Pro
 210 215 220
 Asp Lys Thr Arg Val Gln Arg Lys Gly Ser Arg Gln Arg Val Thr Gly
 225 230 235 240
 Leu Val Val

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 241 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Arg Trp Phe Ala Phe His Arg Glu Val Asp Thr Ala Thr His Tyr Val
 1 5 10 15

Ser Trp Thr Ile Pro Lys Arg Asp Gly Ser Lys Arg Thr Ile Thr Ser
 20 25 30
 Pro Lys Pro Glu Leu Lys Ala Ala Gln Arg Trp Val Leu Ser Asn Val
 35 40 45
 Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly
 50 55 60
 Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val
 65 70 75 80
 Val Lys Val Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Trp Arg Arg
 85 90 95
 Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Arg Glu Gly Thr Ser Thr
 100 105 110
 Leu Leu Ser Leu Leu Ser Thr Glu Ala Pro Arg Glu Ala Val Gln Phe
 115 120 125
 Pro Arg Glu Leu Leu His Val Ala Lys Gly Pro Arg Ala Leu Pro Gln
 130 135 140
 Gly Ala Pro Thr Ser Pro Gly Ile Thr Asn Ala Leu Cys Leu Lys Leu
 145 150 155 160
 Asp Lys Arg Leu Ser Ala Leu Ala Lys Arg Leu Gly Phe Thr Tyr Thr
 165 170 175
 Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Thr Lys Ala Lys Gln Pro
 180 185 190
 Lys Pro Arg Arg Thr Gln Arg Pro Pro Val Ala Val Leu Leu Ser Arg
 195 200 205
 Val Gln Glu Val Val Glu Ala Glu Gly Phe Arg Val His Pro Asp Lys
 210 215 220
 Thr Arg Val Ala Arg Lys Gly Thr Arg Gln Arg Val Thr Gly Leu Val
 225 230 235 240
 Val

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Arg His Tyr Ser Ile His Arg Pro Arg Glu Arg Val Arg His Tyr Val
 1 5 10 15
 Thr Phe Ala Val Pro Lys Arg Ser Gly Gly Val Arg Leu Leu His Ala
 20 25 30
 Pro Lys Arg Arg Leu Lys Ala Leu Gln Arg Arg Met Leu Ala Leu Leu
 35 40 45
 Val Ser Lys Leu Pro Val Ser Pro Gln Ala His Gly Phe Val Pro Gly
 50 55 60
 Arg Ser Ile Lys Thr Gly Ala Ala Pro His Val Gly Arg Arg Val Val
 65 70 75 80
 Leu Lys Leu Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Phe Ala Arg
 85 90 95
 Val Arg Gly Leu Leu Lys Ala Leu Gly Tyr Gly Tyr Pro Val Ala Ala
 100 105 110
 Thr Leu Ala Val Leu Met Thr Glu Ser Glu Arg Gln Pro Val Glu Leu
 115 120 125
 Glu Gly Ile Leu Phe His Val Pro Val Gly Pro Arg Val Cys Val Gln
 130 135 140
 Gly Ala Pro Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu Arg Leu
 145 150 155 160
 Asp Arg Arg Leu Ala Gly Leu Ala Arg Arg Tyr Gly Tyr Thr Tyr Thr
 165 170 175
 Arg Tyr Ala Asp Asp Leu Thr Phe Ser Gly Asp Asp Val Thr Ala Leu
 180 185 190
 Glu Arg Val Arg Ala Leu Ala Ala Arg Tyr Val Gln Glu Glu Gly Phe
 195 200 205
 Glu Val Asn Arg Glu Lys Thr Arg Val Gln Arg Arg Gly Gly Ala Gln
 210 215 220
 Arg Val Thr Gly Val Thr Val
 225 230

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Phe Leu Thr Asn Val Leu Tyr Arg Ile Gly Ser Asp Asn Gln Tyr Thr
 1 5 10 15

Gln Phe Thr Ile Pro Lys Lys Gly Lys Gly Val Arg Thr Ile Ser Ala
 20 25 30
 Pro Thr Asp Arg Leu Lys Asp Ile Gln Arg Arg Ile Cys Asp Leu Leu
 35 40 45
 Ser Asp Cys Arg Asp Glu Ile Phe Ala Ile Arg Lys Ile Ser Asn Asn
 50 55 60
 Tyr Ser Phe Gly Phe Glu Arg Gly Lys Ser Ile Ile Leu Asn Ala Tyr
 65 70 75 80
 Lys His Arg Gly Lys Gln Ile Ile Leu Asn Ile Asp Leu Lys Asp Phe
 85 90 95
 Phe Glu Ser Phe Asn Phe Gly Arg Val Arg Gly Tyr Phe Leu Ser Asn
 100 105 110
 Gln Asp Phe Leu Leu Asn Pro Val Val Ala Thr Thr Leu Ala Lys Ala
 115 120 125
 Ala Cys Tyr Asn Gly Thr Leu Pro Gln Gly Ser Pro Cys Ser Pro Ile
 130 135 140
 Ile Ser Asn Leu Ile Cys Asn Ile Met Asp Met Arg Leu Ala Lys Leu
 145 150 155 160
 Ala Lys Lys Tyr Gly Cys Thr Tyr Ser Arg Tyr Ala Asp Asp Ile Thr
 165 170 175
 Ile Ser Thr Asn Lys Asn Thr Phe Pro Leu Glu Met Ala Thr Val Gln
 180 185 190
 Pro Glu Gly Val Val Leu Gly Lys Val Leu Val Lys Glu Ile Glu Asn
 195 200 205
 Ser Gly Phe Glu Ile Asn Asp Ser Lys Thr Arg Leu Thr Tyr Lys Thr
 210 215 220
 Ser Arg Gln Glu Val Thr Gly Leu Thr Val
 225 230

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 215 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Val Glu Thr Leu Arg Leu Leu Ile Tyr Thr Ala Asp Phe Arg Tyr Arg
 1 5 10 15

Ile Tyr Thr Val Glu Lys Lys Gly Pro Glu Lys Arg Met Arg Thr Ile
 20 25 30
 Tyr Gln Pro Ser Arg Glu Leu Lys Ala Leu Gln Gly Trp Val Leu Arg
 35 40 45
 Asn Ile Leu Asp Lys Leu Ser Ser Ser Pro Phe Ser Ile Gly Phe Glu
 50 55 60
 Lys His Gln Ser Ile Leu Asn Asn Ala Thr Pro His Ile Gly Ala Asn
 65 70 75 80
 Phe Ile Leu Asn Ile Asp Leu Glu Asp Phe Phe Pro Ser Leu Thr Ala
 85 90 95
 Asn Lys Val Phe Gly Val Phe His Ser Leu Gly Tyr Asn Arg Leu Ile
 100 105 110
 Ser Ser Val Leu Thr Lys Ile Cys Cys Tyr Lys Asn Leu Leu Pro Gln
 115 120 125
 Gly Ala Pro Ser Ser Pro Lys Leu Ala Asn Leu Ile Cys Ser Lys Leu
 130 135 140
 Asp Tyr Arg Ile Gln Gly Tyr Ala Gly Ser Arg Gly Leu Ile Tyr Thr
 145 150 155 160
 Arg Tyr Ala Asp Asp Leu Thr Leu Ser Ala Gln Ser Met Lys Lys Val
 165 170 175
 Val Lys Ala Arg Asp Phe Leu Phe Ser Ile Ile Pro Ser Glu Gly Leu
 180 185 190
 Val Ile Asn Ser Lys Lys Thr Cys Ile Ser Gly Pro Arg Ser Gln Arg
 195 200 205
 Lys Val Thr Gly Leu Val Ile
 210 215

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 230 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Thr Lys Gly Phe Ala Ser Glu Val Met Arg Ser Pro Glu Pro Pro Lys
 1 5 10 15
 Lys Trp Asp Ile Ala Lys Lys Lys Gly Gly Met Arg Thr Ile Tyr His
 20 25 30

Pro Ser Ser Lys Val Lys Leu Ile Gln Tyr Trp Leu Met Asn Asn Val
 35 40 45
 Phe Ser Lys Leu Pro Met His Asn Ala Ala Tyr Ala Phe Val Lys Asn
 50 55 60
 Arg Ser Ile Lys Ser Asn Ala Leu Leu His Ala Glu Ser Lys Asn Lys
 65 70 75 80
 Tyr Tyr Val Lys Ile Asp Leu Lys Asp Phe Phe Pro Ser Ile Lys Phe
 85 90 95
 Thr Asp Phe Glu Tyr Ala Phe Thr Arg Tyr Arg Asp Arg Ile Glu Phe
 100 105 110
 Thr Thr Glu Tyr Asp Leu Glu Leu Leu Gln Leu Ile Lys Thr Ile Cys
 115 120 125
 Phe Ile Ser Asp Ser Thr Leu Pro Ile Gly Phe Pro Thr Ser Pro Leu
 130 135 140
 Ile Ala Asn Phe Val Ala Arg Glu Leu Asp Glu Lys Leu Thr Gln Lys
 145 150 155 160
 Leu Asn Ala Ile Asp Lys Leu Asn Ala Thr Tyr Thr Arg Tyr Ala Asp
 165 170 175
 Asp Ile Ile Val Ser Thr Asn Met Lys Gly Ala Ser Lys Leu Ile Leu
 180 185 190
 Asp Cys Phe Lys Arg Thr Met Lys Glu Ile Gly Pro Asp Phe Lys Ile
 195 200 205
 Asn Ile Lys Lys Phe Lys Ile Cys Ser Ala Ser Gly Gly Ser Ile Val
 210 215 220
 Val Thr Gly Leu Lys Val
 225 230

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ile Gln Arg Leu His Ala Leu Ser Asn His Ala Gly Arg His Tyr Arg
 1 5 10 15
 Arg Ile Ile Leu Ser Lys Arg His Gly Gly Gln Arg Leu Val Leu Ala
 20 25 30

Pro Asp Tyr Leu Leu Lys Thr Val Gln Arg Asn Ile Leu Lys Asn Val
 35 40 45
 Leu Ser Gln Phe Pro Leu Ser Pro Phe Ala Thr Ala Tyr Arg Pro Gly
 50 55 60
 Cys Pro Ile Val Ser Asn Ala Gln Pro His Cys Gln Gln Pro Gln Ile
 65 70 75 80
 Leu Lys Leu Asp Ile Glu Asn Phe Phe Asp Ser Ile Ser Trp Leu Gln
 85 90 95
 Val Trp Arg Val Phe Arg Gln Ala Gln Leu Pro Arg Asn Val Val Thr
 100 105 110
 Met Leu Thr Trp Ile Cys Cys Tyr Asn Asp Ala Leu Pro Gln Gly Ala
 115 120 125
 Pro Thr Ser Pro Ala Ile Ser Asn Leu Val Met Arg Arg Phe Asp Glu
 130 135 140
 Arg Ile Gly Glu Trp Cys Gln Ala Arg Gly Ile Thr Tyr Thr Arg Tyr
 145 150 155 160
 Cys Asp Asp Met Thr Phe Ser Gly His Phe Asn Ala Arg Gln Val Lys
 165 170 175
 Asn Lys Val Cys Gly Leu Leu Ala Glu Leu Gly Leu Ser Leu Asn Lys
 180 185 190
 Arg Lys Gly Cys Leu Ile Ala Ala Cys Lys Arg Gln Gln Val Thr Gly
 195 200 205
 Ile Val Val
 210

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 279..1559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CTCCGAGCCC GCCTCCGAGG ACGCGCTCGC GGCCCGGGCG GCGGGGGCGG ACGCGCGGCG	60
GCGGCCCACG GAGACGCTTG ACCCGGGAGA CGACGAATGA CGATAACGGC AGGTGCTCTC	120
GGGAGAGGCC AGGGCTCGCA GATGAGCCAT GAGTACCGCG GTGTTTCGCC GCGGGGGTGT	180
TCTGTCCCA TCTCTTCGCC AGGGTCCCAG CGTACGCAAC GCAGGGAGCC CCGGGTCCAA	240

CGCCTCGCAG GTCGTCCCCT GGCCTCTTCC GGAGCACC ATG AGC TGG TTC GAC	293
Met Ser Trp Phe Asp	
1 5	
ACC ACC CTC TCC CGG CTC AAG GGG TTG TTC AGC CGT CCC GTG ACA CGA	341
Thr Thr Leu Ser Arg Leu Lys Gly Leu Phe Ser Arg Pro Val Thr Arg	
10 15 20	
AGC ACC ACC GGG CTG GAC GTG CCG CTG GAT GCC CAC GGA CGT CCC CAG	389
Ser Thr Thr Gly Leu Asp Val Pro Leu Asp Ala His Gly Arg Pro Gln	
25 30 35	
GAC GTC GTG ACG GAG ACG GTC TCC ACG TCG GGC CCC CTG AAG CCA GGG	437
Asp Val Val Thr Glu Thr Val Ser Thr Ser Gly Pro Leu Lys Pro Gly	
40 45 50	
CAC CTG CGA CAG GTC CGC CGG GAT GCG CGG CTG CTC CCC AAG GGC GTC	485
His Leu Arg Gln Val Arg Arg Asp Ala Arg Leu Leu Pro Lys Gly Val	
55 60 65	
CGC CGC TAC ACC CCG GGC CGG AAG AAG TGG ATG GAG GCC GCC GAG GCC	533
Arg Arg Tyr Thr Pro Gly Arg Lys Lys Trp Met Glu Ala Ala Glu Ala	
70 75 80 85	
CGG CGG CTG TTC TCC GCC ACG CTG CGC ACG CGG AAC CGG AAC CTG AGG	581
Arg Arg Leu Phe Ser Ala Thr Leu Arg Thr Arg Asn Arg Asn Leu Arg	
90 95 100	
GAC TTG CTG CCC GAC GAG GCA CAG CTG GCG CGC TAC GGC CTG CCG GTC	629
Asp Leu Leu Pro Asp Glu Ala Gln Leu Ala Arg Tyr Gly Leu Pro Val	
105 110 115	
TGG CGC ACG GAA GAG GAC GTG GCA GCG GCC CTG GGC GTC TCG GTG GGC	677
Trp Arg Thr Glu Glu Asp Val Ala Ala Ala Leu Gly Val Ser Val Gly	
120 125 130	
GTG CTC CGC CAC TAC AGC ATC CAC CGC CCG CGC GAG CGG GTG CGG CAC	725
Val Leu Arg His Tyr Ser Ile His Arg Pro Arg Glu Arg Val Arg His	
135 140 145	
TAC GTG ACC TTC GCC GTG CCC AAG CGC TCC GGA GGC GTC CGG CTG CTG	773
Tyr Val Thr Phe Ala Val Pro Lys Arg Ser Gly Gly Val Arg Leu Leu	
150 155 160 165	
CAT GCG CCC AAG CGG CGC CTG AAG GCC CTG CAA CGC CGG ATG CTG GCG	821
His Ala Pro Lys Arg Arg Leu Lys Ala Leu Gln Arg Arg Met Leu Ala	
170 175 180	
CTC CTG GTG TCG AAG CTC CCC GTG AGT CCA CAG GCC CAT GGC TTC GTG	869
Leu Leu Val Ser Lys Leu Pro Val Ser Pro Gln Ala His Gly Phe Val	
185 190 195	
CCC GGC CGC TCC ATC AAG ACG GGC GCC GCG CCG CAC GTG GGC CGG CGG	917
Pro Gly Arg Ser Ile Lys Thr Gly Ala Ala Pro His Val Gly Arg Arg	
200 205 210	
GTG GTC CTG AAG CTG GAC CTG AAG GAC TTC TTC CCC TCC GTC ACC TTC	965
Val Val Leu Lys Leu Asp Leu Lys Asp Phe Phe Pro Ser Val Thr Phe	
215 220 225	

GCG CGG GTG CGA GGG CTG CTC ATC GCC CTG GGC TAC GGC TAT CCC GTG Ala Arg Val Arg Gly Leu Ile Ala Leu Gly Tyr Gly Tyr Pro Val 230 235 240 245	1013
GCG GCC ACG CTC GCG GTG CTG ATG ACG GAG TCC GAG CGC CAG CCC GTG Ala Ala Thr Leu Ala Val Leu Met Thr Glu Ser Glu Arg Gln Pro Val 250 255 260	1061
GAG CTG GAG GGC ATC CTC TTC CAC GTT CCC GTG GGC CCA CGC GTC TGC Glu Leu Glu Gly Ile Leu Phe His Val Pro Val Gly Pro Arg Val Cys 265 270 275	1109
GTG CAG GGC GCC CCC ACG AGC CCC GCC CTG TGC AAC GCG GTG CTG CTG Val Gln Gly Ala Pro Thr Ser Pro Ala Leu Cys Asn Ala Val Leu Leu 280 285 290	1157
CGA CTG GAC CGG CGG CTG GCG GGA CTG GCG CGT CGG TAC GGC TAC ACG Arg Leu Asp Arg Arg Leu Ala Gly Leu Ala Arg Arg Tyr Gly Tyr Thr 295 300 305	1205
TAC ACG CGC TAC GCG GAT GAC CTC ACC TTC TCC GGC GAC GAC GTC ACG Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Gly Asp Asp Val Thr 310 315 320 325	1253
GCG CTG GAG CGA GTC CGC GCG CTG GCC GCG CGG TAC GTG CAG GAG GAA Ala Leu Glu Arg Val Arg Ala Leu Ala Ala Arg Tyr Val Gln Glu Glu 330 335 340	1301
GGC TTC GAG GTC AAC CGC GAG AAG ACC CGC GTG CAG CGC CGG GGC GGT Gly Phe Glu Val Asn Arg Glu Lys Thr Arg Val Gln Arg Arg Gly Gly 345 350 355	1349
GCC CAG CGC GTC ACT GGC GTC ACC GTG AAT ACG ACG CTG GGC TTG TCA Ala Gln Arg Val Thr Gly Val Thr Val Asn Thr Thr Leu Gly Leu Ser 360 365 370	1397
CGC GAG GAG CGG CCG CGG CTC CGG GCG ATG CTG CAC CAG GAG GCG CGG Arg Glu Glu Arg Pro Arg Leu Arg Ala Met Leu His Gln Glu Ala Arg 375 380 385	1445
TCG GAG GAC GTC GAG GCA CAC CGC GCG CAC CTC GAC GGC CTC CTG GCC Ser Glu Asp Val Glu Ala His Arg Ala His Leu Asp Gly Leu Leu Ala 390 395 400 405	1493
TAC GTG AAG ATG CTC AAC CCG GAG CAG GCG GAG CGG CTC GCT CGC CGG Tyr Val Lys Met Leu Asn Pro Glu Gln Ala Glu Arg Leu Ala Arg Arg 410 415 420	1541
CGC AAG CCG CGC GGG ACG TGAGCGAGGG CTCAGCTCCG GATGGGCCAG Arg Lys Pro Arg Gly Thr 425	1589
GGCCTGTCAC GCGTCCCGGC CTCCCAGTTG TCATGGCGGC CGTCCCAGTA C	1640

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 427 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met Ser Trp Phe Asp Thr Thr Leu Ser Arg Leu Lys Gly Leu Phe Ser
1 5 10 15
Arg Pro Val Thr Arg Ser Thr Thr Gly Leu Asp Val Pro Leu Asp Ala
20 25 30
His Gly Arg Pro Gln Asp Val Val Thr Glu Thr Val Ser Thr Ser Gly
35 40 45
Pro Leu Lys Pro Gly His Leu Arg Gln Val Arg Arg Asp Ala Arg Leu
50 55 60
Leu Pro Lys Gly Val Arg Arg Tyr Thr Pro Gly Arg Lys Lys Trp Met
65 70 75 80
Glu Ala Ala Glu Ala Arg Arg Leu Phe Ser Ala Thr Leu Arg Thr Arg
85 90 95
Asn Arg Asn Leu Arg Asp Leu Leu Pro Asp Glu Ala Gln Leu Ala Arg
100 105 110
Tyr Gly Leu Pro Val Trp Arg Thr Glu Glu Asp Val Ala Ala Ala Leu
115 120 125
Gly Val Ser Val Gly Val Leu Arg His Tyr Ser Ile His Arg Pro Arg
130 135 140
Glu Arg Val Arg His Tyr Val Thr Phe Ala Val Pro Lys Arg Ser Gly
145 150 155 160
Gly Val Arg Leu Leu His Ala Pro Lys Arg Arg Leu Lys Ala Leu Gln
165 170 175
Arg Arg Met Leu Ala Leu Leu Val Ser Lys Leu Pro Val Ser Pro Gln
180 185 190
Ala His Gly Phe Val Pro Gly Arg Ser Ile Lys Thr Gly Ala Ala Pro
195 200 205
His Val Gly Arg Arg Val Val Leu Lys Leu Asp Leu Lys Asp Phe Phe
210 215 220
Pro Ser Val Thr Phe Ala Arg Val Arg Gly Leu Leu Ile Ala Leu Gly
225 230 235 240
Tyr Gly Tyr Pro Val Ala Ala Thr Leu Ala Val Leu Met Thr Glu Ser
245 250 255
Glu Arg Gln Pro Val Glu Leu Glu Gly Ile Leu Phe His Val Pro Val
260 265 270
Gly Pro Arg Val Cys Val Gln Gly Ala Pro Thr Ser Pro Ala Leu Cys
275 280 285
Asn Ala Val Leu Leu Arg Leu Asp Arg Arg Leu Ala Gly Leu Ala Arg
290 295 300

Arg Tyr Gly Tyr Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser
 305 310 315 320
 Gly Asp Asp Val Thr Ala Leu Glu Arg Val Arg Ala Leu Ala Ala Arg
 325 330 335
 Tyr Val Gln Glu Glu Gly Phe Glu Val Asn Arg Glu Lys Thr Arg Val
 340 345 350
 Gln Arg Arg Gly Gly Ala Gln Arg Val Thr Gly Val Thr Val Asn Thr
 355 360 365
 Thr Leu Gly Leu Ser Arg Glu Glu Arg Pro Arg Leu Arg Ala Met Leu
 370 375 380
 His Gln Glu Ala Arg Ser Glu Asp Val Glu Ala His Arg Ala His Leu
 385 390 395 400
 Asp Gly Leu Leu Ala Tyr Val Lys Met Leu Asn Pro Glu Gln Ala Glu
 405 410 415
 Arg Leu Ala Arg Arg Arg Lys Pro Arg Gly Thr
 420 425

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3060 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 763..2202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCCACTTCCG GCGCTCGGGC TGCGCGAGGG CCCGTGCGAG CACATGATGG CGCTGCGGCT	60
CGTCCAGGTC CGGCACCGCG CCGAGCAGGA AGCACTGCGT CAGACCCCCG CGGGCCGCCA	120
GCTCATCCGC GCGGAGACGC GCTCCTACGT GCGGCGCGAG CCCTCCGGCC AGGAGCAGGT	180
GTACCGCGTC TCATTGGATG GGAAAGTGGT GGCGGTGGAG TGGGGCCCCC GCCAGGGGGA	240
GTCCCGCCGG CAGAAGCTCT GGTTCGACAC GGACCCGAG GCGCGCACCG CCTACTTCAC	300
GCGCCTGGAG TCCTTGCCG CGGAGGGATA TATCGATGCG GCTGCTTCAA TGATGTAGAA	360
CACGCAAGCC ACGGGGCCGC GGGCGCGCGG CGGAAAGGCA GGTGCGACGG AACGACAGAC	420
ACTCGTGCGA GCGACCGAGA GAGGTCCCAA GCCATCAGCC TCAGCGCCTC GAGCGCGAGA	480
GCGGCGTTGC GCCGCTCTGG TTGAATTGCA GGACACTCTC CGCAAGGTAG CCTGTTCTTG	540

GCTCTCTTCC CTCCGGTGAG TACCTCTCCG GCCGGGGAGC TGAACCAACG ACGCAACCGC	600
CGTTTCCCCG GCCGGAGAGG TACTCACCGG AGGGGAGAGC CGGTGAGGCT ACCGTGCCCC	660
AGGTGAGAAG GTGGTGCTT CGGGCCTCCC TCGACCGCTC GCGCTCCGTC GCCCTGCCCT	720
GCCTCGCCCC CCCACCTTG CTCACCGGCG CCAGGAGCCG TC ATG ACC GCC AAG	774
Met Thr Ala Lys	
1	
CTG GAG TCA CAC GTC CCC GCC GCG CCC CCC GTC TCC GCC GAG GCG CCC	822
Leu Glu Ser His Val Pro Ala Ala Pro Pro Val Ser Ala Glu Ala Pro	
5 10 15 20	
GCC CCC ACC CGT CCC GAT GCC GCG AAG CAG GAG GCC CGC CGC GCC CAC	870
Ala Pro Thr Arg Pro Asp Ala Ala Lys Gln Glu Ala Arg Arg Ala His	
25 30 35	
CAC GAG GCG CTG CGC CTG CGG TGG AAG GCC ATC GAA GAG GCG GGC GGC	918
His Glu Ala Leu Arg Leu Arg Trp Lys Ala Ile Glu Glu Ala Gly Gly	
40 45 50	
ACG GAC GCC TGG GTG CGG CAG CAG CTG GTG GCC AAG GGC GTC GCG GCG	966
Thr Asp Ala Trp Val Arg Gln Gln Leu Val Ala Lys Gly Val Ala Ala	
55 60 65	
GAA GAG GTG GAC TTC GAG TCG CTC AGC GAC AAG CAG AAG GCG GCC TGG	1014
Glu Glu Val Asp Phe Glu Ser Leu Ser Asp Lys Gln Lys Ala Ala Trp	
70 75 80	
AAG GAG AAG AAG AAG GCC GAG GCC ACC GAG CGG CGC GCG CAG AAG CGC	1062
Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg Ala Gln Lys Arg	
85 90 95 100	
CTG GCG TGG GAG GCC TGG AAG GCC ACG CAC ATC CAC CAC CTG GGC GTG	1110
Leu Ala Trp Glu Ala Trp Lys Ala Thr His Ile His His Leu Gly Val	
105 110 115	
GGG GTG CAC TGG GAC GAG GCC GGA GGG CCG GAC AAG TTC GAC GTG GCC	1158
Gly Val His Trp Asp Glu Ala Gly Gly Pro Asp Lys Phe Asp Val Ala	
120 125 130	
GGG CGC GAG GAG CGG GCC AAG GCC AAC GGC TTG CCG GAG GGC TTG GAC	1206
Gly Arg Glu Glu Arg Ala Lys Ala Asn Gly Leu Pro Glu Gly Leu Asp	
135 140 145	
TCG GTC GAG GCG CTG GCC AAA GCG CTG GGC ATC TCC GTG TCG CGC CTG	1254
Ser Val Glu Ala Leu Ala Lys Ala Leu Gly Ile Ser Val Ser Arg Leu	
150 155 160	
CGC TGG TTC TCC TTC CAC CGC GAG GTG GAC ACG GGC ACG CAC TAC CAG	1302
Arg Trp Phe Ser Phe His Arg Glu Val Asp Thr Gly Thr His Tyr Gln	
165 170 175 180	
ACG TGG GAG ATT CCG AAG CGG GAC GGC GGC AAG CGG ACG CTC ACC GCG	1350
Thr Trp Glu Ile Pro Lys Arg Asp Gly Gly Lys Arg Thr Leu Thr Ala	
185 190 195	
CCG AAG CGG GAG CTC AAG GCC GTG CAG CGC TGG GTG CTC GCG AAC GTG	1398
Pro Lys Arg Glu Leu Lys Ala Val Gln Arg Trp Val Leu Ala Asn Val	
200 205 210	

GTG GAG CGG CTG CCG GTG CAC GGG GCC GCG CAC GGC TTC GTG GCG GGG Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly Phe Val Ala Gly 215 220 225	1446
CGC TCC ATC CTC ACC AAC GCG CTG GCC CAC CAG GGC GCG GAC GTG GTG Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly Ala Asp Val Val 230 235 240	1494
GTG AAG GTG GAC ATG AAG GAC TTC TTC CCT TCC GTG ACG TGG CCC CGG Val Lys Val Asp Met Lys Asp Phe Phe Pro Ser Val Thr Trp Pro Arg 245 250 255 260	1542
GTC AAG GGA CTG CTG CGC AAG GGA GGA CTC CCG GAG AAC CTG GCG ACG Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Pro Glu Asn Leu Ala Thr 265 270 275	1590
CTC CTG GCG CTG CTC TCC ACC GAG GCC CCG CGC GAG GTG GTG CGG TTC Leu Leu Ala Leu Leu Ser Thr Glu Ala Pro Arg Glu Val Val Arg Phe 280 285 290	1638
CGG GGA GAG ACG CTG TAC GTG GCC AAG GGC CCT CGC GCG CTG CCC CAG Arg Gly Glu Thr Leu Tyr Val Ala Lys Gly Pro Arg Ala Leu Pro Gln 295 300 305	1686
GGG GCC CCC ACC TCT CCG GCG CTG ACG AAC GCG CTG TGC CTG CGG CTG Gly Ala Pro Thr Ser Pro Ala Leu Thr Asn Ala Leu Cys Leu Arg Leu 310 315 320	1734
GAC AAG CGG CTC TCG GCG CTG TCG AAG CGG CTG GGC TTC ACG TAC ACG Asp Lys Arg Leu Ser Ala Leu Ser Lys Arg Leu Gly Phe Thr Tyr Thr 325 330 335 340	1782
CGC TAT GCG GAT GAC CTG ACG TTC TCC TGG CGG CGG GCG AAG AAG TCC Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Arg Arg Ala Lys Lys Ser 345 350 355	1830
CGG CAG AAG GAA CTC CCC CTG GCG GAT GCG CCG GTG GCG CTG CTC CTG Arg Gln Lys Glu Leu Pro Leu Ala Asp Ala Pro Val Ala Leu Leu Leu 360 365 370	1878
GCG CGG GTG AAG GGT GTG CTG GAG GCC GAG GGT TTC ACG CTG CAC CCG Ala Arg Val Lys Gly Val Leu Glu Ala Glu Gly Phe Thr Leu His Pro 375 380 385	1926
GAC AAG ACG CGG GTG CAG CGC AAG GGC AGC CGG CAG CGG GTG ACG GGG Asp Lys Thr Arg Val Gln Arg Lys Gly Ser Arg Gln Arg Val Thr Gly 390 395 400	1974
CTC GTG GTG AAC GAG GCC CCC GAG GGC GTT CCG GGT GCC CGG GTG CCC Leu Val Val Asn Glu Ala Pro Glu Gly Val Pro Gly Ala Arg Val Pro 405 410 415 420	2022
CGC GAT GTG GTG CGG CGG CTG CGC GCG GCG ATC CAC AAC CGG GAG CAG Arg Asp Val Val Arg Arg Leu Arg Ala Ala Ile His Asn Arg Glu Gln 425 430 435	2070
GGC AAG CCC GGC CCC ACC GGG GAG ACG CTG GAG CAG CTC AAG GGG CTC Gly Lys Pro Gly Pro Thr Gly Glu Thr Leu Glu Gln Leu Lys Gly Leu 440 445 450	2118

GCG GCC TTC CTT CAC ATG ACG GAC GCG GAG AAG GGC CGC GCC TTC CTG Ala Ala Phe Leu His Met Thr Asp Ala Glu Lys Gly Arg Ala Phe Leu 455 460 465	2166
CGA CGG CTG GAG GCC CTC GAG AAG CGC CAG ACC GCC TGACCCTCAC Arg Arg Leu Glu Ala Leu Glu Lys Arg Gln Thr Ala 470 475 480	2212
TGGTCGTCGG GGGCATCGCA GCGGGCGCCG GGACGGACCG TCACCCCCCA GATCTCCATG	2272
CCATGCTGGG GATTCTGGGC GGTGAAGAAG ACTTCCCAGC CGAGACGGAC GAAGCCCTGC	2332
GGATCCGATG ACTCCTCGCC CGGGGCGATC TCCCGGAGGG GCACCGTTCC GACGTCCGTG	2392
CCATTGCTCA CCCAGGGCTC CCGGCCCCAG CCTTGGGTGT CCGCCGAGAA GAAGAGCAGC	2452
CCGGAGATGG CCGTCAGGTT CTCCGGCGAC GCATCCTCGG GGCCCGGCGC CAAATCCTTC	2512
AGCAGCAGGG TGCCCTTGGC GGTGCCATCG CTGGACCACA GCTCCCGGCC GTGGAGGCTG	2572
TCACTCGCGG CGAAGTAGAG CATCCCATTG AGCGCCTTGA TGGCGCTGGG CGCCGAGCTG	2632
TCCGGACCCG GCCAGATGTC CTTACCCCGG ACCGTGCCAT GCGACGTGCC ATCGCTGACC	2692
CACAGCTCCT CGCCCTCGGG CTGGCCCCAG AACTCGGGCT CGCCTCCCCC GGCGCTGAAG	2752
AAGATCTTCC CCCCAGAGCG CGTGAGATCA TGCGGATAGA GGCCGGGGAA GAAGCGCAGC	2812
TGCTCGGAGA CGGTGCCTCT GGAGCACCAC AGGCTGGCCT CGCCTTCGTC ATTGTCGAGC	2872
AGGAAGAAGA GCACCGAGTC CGCCGCGGTG AACGCGGAGA GGAAGTTGTC CTCGGGGCCC	2932
GTGAAGACAG ACGTGGTGCT GGACAGCCCC AGGCTGCGCC AGATGAACAC CTCGTCATTG	2992
ACGTTGGCCA CGAAGAAGAG CGCATCGCCG ACCCGGGTGA GCCGGCGCGG GCTGGAGCTG	3052
CCGGGCAC	3060

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 480 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Thr Ala Lys Leu Glu Ser His Val Pro Ala Ala Pro Pro Val Ser 1 5 10 15
Ala Glu Ala Pro Ala Pro Thr Arg Pro Asp Ala Ala Lys Gln Glu Ala 20 25 30
Arg Arg Ala His His Glu Ala Leu Arg Leu Arg Trp Lys Ala Ile Glu 35 40 45
Glu Ala Gly Gly Thr Asp Ala Trp Val Arg Gln Gln Leu Val Ala Lys 50 55 60

Gly Val Ala Ala Glu Glu Val Asp Phe Glu Ser Leu Ser Asp Lys Gln
 65 70 75 80
 Lys Ala Ala Trp Lys Glu Lys Lys Lys Ala Glu Ala Thr Glu Arg Arg
 85 90 95
 Ala Gln Lys Arg Leu Ala Trp Glu Ala Trp Lys Ala Thr His Ile His
 100 105 110
 His Leu Gly Val Gly Val His Trp Asp Glu Ala Gly Gly Pro Asp Lys
 115 120 125
 Phe Asp Val Ala Gly Arg Glu Glu Arg Ala Lys Ala Asn Gly Leu Pro
 130 135 140
 Glu Gly Leu Asp Ser Val Glu Ala Leu Ala Lys Ala Leu Gly Ile Ser
 145 150 155 160
 Val Ser Arg Leu Arg Trp Phe Ser Phe His Arg Glu Val Asp Thr Gly
 165 170 175
 Thr His Tyr Gln Thr Trp Glu Ile Pro Lys Arg Asp Gly Gly Lys Arg
 180 185 190
 Thr Leu Thr Ala Pro Lys Arg Glu Leu Lys Ala Val Gln Arg Trp Val
 195 200 205
 Leu Ala Asn Val Val Glu Arg Leu Pro Val His Gly Ala Ala His Gly
 210 215 220
 Phe Val Ala Gly Arg Ser Ile Leu Thr Asn Ala Leu Ala His Gln Gly
 225 230 235 240
 Ala Asp Val Val Val Lys Val Asp Met Lys Asp Phe Phe Pro Ser Val
 245 250 255
 Thr Trp Pro Arg Val Lys Gly Leu Leu Arg Lys Gly Gly Leu Pro Glu
 260 265 270
 Asn Leu Ala Thr Leu Leu Ala Leu Leu Ser Thr Glu Ala Pro Arg Glu
 275 280 285
 Val Val Arg Phe Arg Gly Glu Thr Leu Tyr Val Ala Lys Gly Pro Arg
 290 295 300
 Ala Leu Pro Gln Gly Ala Pro Thr Ser Pro Ala Leu Thr Asn Ala Leu
 305 310 315 320
 Cys Leu Arg Leu Asp Lys Arg Leu Ser Ala Leu Ser Lys Arg Leu Gly
 325 330 335
 Phe Thr Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Phe Ser Trp Arg Arg
 340 345 350
 Ala Lys Lys Ser Arg Gln Lys Glu Leu Pro Leu Ala Asp Ala Pro Val
 355 360 365
 Ala Leu Leu Leu Ala Arg Val Lys Gly Val Leu Glu Ala Glu Gly Phe
 370 375 380

Thr Leu His Pro Asp Lys Thr Arg Val Gln Arg Lys Gly Ser Arg Gln
 385 390 395 400
 Arg Val Thr Gly Leu Val Val Asn Glu Ala Pro Glu Gly Val Pro Gly
 405 410 415
 Ala Arg Val Pro Arg Asp Val Val Arg Arg Leu Arg Ala Ala Ile His
 420 425 430
 Asn Arg Glu Gln Gly Lys Pro Gly Pro Thr Gly Glu Thr Leu Glu Gln
 435 440 445
 Leu Lys Gly Leu Ala Ala Phe Leu His Met Thr Asp Ala Glu Lys Gly
 450 455 460
 Arg Ala Phe Leu Arg Arg Leu Glu Ala Leu Glu Lys Arg Gln Thr Ala
 465 470 475 480

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2788 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: join(2..103, 707..1654)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

T TTC GAG AAG CGC CAT ACC AAA CAG GGG ATA CAG ACC AAC CTG ACG	46
Phe Glu Lys Arg His Thr Lys Gln Gly Ile Gln Thr Asn Leu Thr	
1 5 10 15	
CTG AAA GAG GAA AGC TAC GGC GAC TGG CTG CCG AAG TGC GAC GAC CCC	94
Leu Lys Glu Glu Ser Tyr Gly Asp Trp Leu Pro Lys Cys Asp Asp Pro	
20 25 30	
GCA GCA ACA TAACCTCACT CAGACCGGCA ACAGCCGGTC TTTTCCTTTC	143
Ala Ala Thr	
TGGCCATTGC CACAAGGTGA ACAATCCACT GTTACCCTT CACCGTTTAT TCACCCTTTA	203
TCACTATGAA ATTATTAATA AAAAACCAGA GGTGAACAGT GTGAACAGTA AAACCTGAAA	263
AAACTTTTTTA TCACCCCGCG CATCGCCCGA CTGGACAGAT CCAGAACGAG CAAAAATCAC	323
AAAGGTGACG AGTCGACTGT TCACTCTTCA CCAACTCATC ACCACCTAAC CACATGATAT	383
AAAATGATAA ATAATCGAGG TGAACAGTTA AATGCAAAAA AACTTTTTCT CAGCTCTTGG	443
ATAAAAGAAA ATTAATTCAC ATCAATAGCT TTCCTCTTGA ATCCTCTTGA GGTTTATGAG	503

AGCGTAACAG AGCCAAACCT AGCATTTTAT GGGTTAATAG CCCATCGCGC ATGAGTCATG	563
GTTTCGCCTA GTATTTTAGC TATGCCCGTC GTTCAGTTCG CTGAGCGGCG GCTGGGGGCC	623
ACCGATCAGC GAACTGATCG ACGTGCTCAA GTAGGTTTGG CTCTTTTAGT CCTCTACCAT	683
CAAGGTGCAT AAGGATATTC TCG ATG CTG ACT CAG CTA AAA AAA AAT GGT	733
Met Leu Thr Gln Leu Lys Lys Asn Gly	
35 40	
ACT GAG GTA TCT AGA GCA ACC GCG TTA TTT TCA TCA TTC GTT GAA AAG	781
Thr Glu Val Ser Arg Ala Thr Ala Leu Phe Ser Ser Phe Val Glu Lys	
45 50 55	
AAC AAA GTA AAA TGT CCT GGT AAT GTA AAA AAA TTC GTC TTT CTG TGT	829
Asn Lys Val Lys Cys Pro Gly Asn Val Lys Lys Phe Val Phe Leu Cys	
60 65 70 75	
GGT GCT AAC AAA AAC AAT GGA GAA CCA TCA GCA AGA CGA TTG GAA TTA	877
Gly Ala Asn Lys Asn Asn Gly Glu Pro Ser Ala Arg Arg Leu Glu Leu	
80 85 90	
ATA AAT TTT TCT GAA AGG TAT TTG AAT AAC TGT CAC TTT TTT CTT GCT	925
Ile Asn Phe Ser Glu Arg Tyr Leu Asn Asn Cys His Phe Phe Leu Ala	
95 100 105	
GAA CTA GTT TTC AAA GAA TTA AGC ACC GAT GAA GAA TCA TTA TCT GAT	973
Glu Leu Val Phe Lys Glu Leu Ser Thr Asp Glu Glu Ser Leu Ser Asp	
110 115 120	
AAT TTA TTA GAT ATC GAA GCT GAC TTA TCT AAA TTA GCT GAT CAT ATT	1021
Asn Leu Leu Asp Ile Glu Ala Asp Leu Ser Lys Leu Ala Asp His Ile	
125 130 135	
ATC ATT GTT TTA GAA AGT TAT TCA TCT TTC ACG GAA CTT GGT GCA TTC	1069
Ile Ile Val Leu Glu Ser Tyr Ser Ser Phe Thr Glu Leu Gly Ala Phe	
140 145 150 155	
GCA TAC AGC AAG CAA TTA CGC AAG AAA TTA ATA ATA GTT AAC AAT ACA	1117
Ala Tyr Ser Lys Gln Leu Arg Lys Lys Leu Ile Ile Val Asn Asn Thr	
160 165 170	
AAA TTT ATA AAT GAG AAA TCA TTT ATA AAT ATG GGA CCA ATA AAG GCT	1165
Lys Phe Ile Asn Glu Lys Ser Phe Ile Asn Met Gly Pro Ile Lys Ala	
175 180 185	
ATT ACT CAG CAA TCA CAA CAA TCT GGT CAT TTC TTA CAT TAT AAA ATG	1213
Ile Thr Gln Gln Ser Gln Gln Ser Gly His Phe Leu His Tyr Lys Met	
190 195 200	
ACA GAA GGT ATT GAA AGT ATA GAG CGC TCT GAT GGG ATT GGC GAA ATA	1261
Thr Glu Gly Ile Glu Ser Ile Glu Arg Ser Asp Gly Ile Gly Glu Ile	
205 210 215	
TTC GAC CCC CTA TAT GAT ATT CTT TCT AAG AAC GAC AGA GCA ATT TCA	1309
Phe Asp Pro Leu Tyr Asp Ile Leu Ser Lys Asn Asp Arg Ala Ile Ser	
220 225 230 235	
AGA ACT TTA AAA AAA GAA GAG TTA GAT CCT TCC AGT AAC TTC AAT AAA	1357
Arg Thr Leu Lys Lys Glu Glu Leu Asp Pro Ser Ser Asn Phe Asn Lys	
240 245 250	

GAC TCA GTA CGA TTT ATT CAT GAC GTA ATT TTT GTA TGT GGT CCT TTG	1405
Asp Ser Val Arg Phe Ile His Asp Val Ile Phe Val Cys Gly Pro Leu	
255 260 265	
CAA CTT AAT GAA CTC ATC GAA ATA ATC ACA AAA ATA TTT GGC ACA GAA	1453
Gln Leu Asn Glu Leu Ile Glu Ile Ile Thr Lys Ile Phe Gly Thr Glu	
270 275 280	
AGC CAT TAC AAA AAA AAT CTT CTA AAG CAC CTT GGT ATT CTA ATA GCT	1501
Ser His Tyr Lys Lys Asn Leu Leu Lys His Leu Gly Ile Leu Ile Ala	
285 290 295	
ATT AGA ATA ATA TCA TGC ACA AAT GGG ATT TAT TAT TCT TTG TAT AAA	1549
Ile Arg Ile Ile Ser Cys Thr Asn Gly Ile Tyr Tyr Ser Leu Tyr Lys	
300 305 310 315	
GAA TAT TAT TTT AAA TAT GAC TTT GAC ATT GAC AAC ATA TCA TCA ATG	1597
Glu Tyr Tyr Phe Lys Tyr Asp Phe Asp Ile Asp Asn Ile Ser Ser Met	
320 325 330	
TTT AAA GTT TTT TTC CTC AAG AAC AAG CCA GAA AGG ATG AGG GTA TAT	1645
Phe Lys Val Phe Phe Leu Lys Asn Lys Pro Glu Arg Met Arg Val Tyr	
335 340 345	
GAG AAT ATA TAGCCTAATT GATTCTCAGA CATTGATGAC TAAGGGATT	1694
Glu Asn Ile	
350	
GCTTCTGAAG TAATGCGATC ACCTGAGCCG CCAAAAAAAT GGGATATAGC TAAGAAAAAA	1754
GGAGGTATGA GAACAATTTA TCACCCGTCA TCAAAAGTTA AATTAATTCA ATATTGGTTA	1814
ATGAATAATG TTTTTTCGAA GCTCCCAATG CATAATGCTG CATATGCATT TGTAAAAAAC	1874
CGATCAATAA AAAGCAATGC TTTATTACAT GCCGAATCAA AGAATAAGTA TTATGTGAAA	1934
ATAGATCTCA AAGATTTTTT CCCTTCAATA AAATTTACTG ATTTTGAGTA CGCATTCACT	1994
CGTTATCGAG ATCGCATTGA ATTTACTACA GAATATGATA AGGAGTTACT ACAACTTATA	2054
AAAACGATCT GCTTTATATC AGATAGCACT CTCCCTATCG GGTTTCCTAC ATCTCCATTA	2114
ATTGCAAAC TGTGGCAAG AGAACTTGAT GAAAAACTGA CGCAAAAACT AAATGCAATT	2174
GATAAACTTA ATGCCACTTA TACACGATAT GCTGATGATA TTATTGTCTC TACAAATATG	2234
AAAGGGGCTA GCAAATTAAT TCTGGATTGT TTTAAAAGAA CAATGAAAGA GATTGGTCCA	2294
GACTTTAAAA TTAACATTAA AAAATTTAAG ATTTGTAGTG CTTCGGGAGG AAGTATAGTA	2354
GTTACCGGAT TGAAAGTTTG CCACGATTTT CATATTACAT TACATAGATC AATGAAAGAT	2414
AAAATAAGAT TGCATCTTTC TCTTTTATCA AAGGGCATAT TAAAAGATGA AGATCATAAT	2474
AAACTTTCTG GTTATATTGC TTATGCAAAA GATATAGACC CTCATTTTTA TACAAAAC TG	2534
AACAGAAAAT ATTTTCAAGA AATAAAATGG ATTCAGAATC TCCACAACAA AGTTGAATAA	2594
ACTTTATATT TTGGATGCAC CCCAATAACT TCATTGATTA AATTGGGAAC AATATAGGCT	2654

TTTCAGGATG ACCTACACTC TAGAGAA'
 CCTATATAAA ATACAGCAAA ATCAATGC
 CGCCAAAATG CCTC

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Glu Lys Arg His Thr Lys Gln Gly Ile Gln Thr Asn Leu Thr Leu
 1 5 10 15
 Lys Glu Glu Ser Tyr Gly Asp Trp Leu Pro Lys Cys Asp Asp Pro Ala
 20 25 30
 Ala Thr Met Leu Thr Gln Leu Lys Lys Asn Gly Thr Glu Val Ser Arg
 35 40 45
 Ala Thr Ala Leu Phe Ser Ser Phe Val Glu Lys Asn Lys Val Lys Cys
 50 55 60
 Pro Gly Asn Val Lys Lys Phe Val Phe Leu Cys Gly Ala Asn Lys Asn
 65 70 75 80
 Asn Gly Glu Pro Ser Ala Arg Arg Leu Glu Leu Ile Asn Phe Ser Glu
 85 90 95
 Arg Tyr Leu Asn Asn Cys His Phe Phe Leu Ala Glu Leu Val Phe Lys
 100 105 110
 Glu Leu Ser Thr Asp Glu Glu Ser Leu Ser Asp Asn Leu Leu Asp Ile
 115 120 125
 Glu Ala Asp Leu Ser Lys Leu Ala Asp His Ile Ile Ile Val Leu Glu
 130 135 140
 Ser Tyr Ser Ser Phe Thr Glu Leu Gly Ala Phe Ala Tyr Ser Lys Gln
 145 150 155 160
 Leu Arg Lys Lys Leu Ile Ile Val Asn Asn Thr Lys Phe Ile Asn Glu
 165 170 175
 Lys Ser Phe Ile Asn Met Gly Pro Ile Lys Ala Ile Thr Gln Gln Ser
 180 185 190
 Gln Gln Ser Gly His Phe Leu His Tyr Lys Met Thr Glu Gly Ile Glu
 195 200 205
 Ser Ile Glu Arg Ser Asp Gly Ile Gly Glu Ile Phe Asp Pro Leu Tyr
 210 215 220

GT TATTTTCAAA
 TGTGATCTTC

2714

2774

2788

Asp Ile Leu Ser Lys Asn Asp Arg Ala
225 230

Glu Glu Leu Asp Pro Ser Ser Asn Phe A
245 250

Ile His Asp Val Ile Phe Val Cys Gly Pro Leu Gln Lys
260 265 240

Ile Glu Ile Ile Thr Lys Ile Phe Gly Thr Glu Ser His Tyr Lys
275 280 285

Asn Leu Leu Lys His Leu Gly Ile Leu Ile Ala Ile Arg Ile Ile Ser
290 295 300

Cys Thr Asn Gly Ile Tyr Tyr Ser Leu Tyr Lys Glu Tyr Tyr Phe Lys
305 310 315 320

Tyr Asp Phe Asp Ile Asp Asn Ile Ser Ser Met Phe Lys Val Phe Phe
325 330 335

Leu Lys Asn Lys Pro Glu Arg Met Arg Val Tyr Glu Asn Ile
340 345 350

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 316 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Arg Ile Tyr Ser Leu Ile Asp Ser Gln Thr Leu Met Thr Lys Gly
1 5 10 15

Phe Ala Ser Glu Val Met Arg Ser Pro Glu Pro Pro Lys Lys Trp Asp
20 25 30

Ile Ala Lys Lys Lys Gly Gly Met Arg Thr Ile Tyr His Pro Ser Ser
35 40 45

Lys Val Lys Leu Ile Gln Tyr Trp Leu Met Asn Asn Val Phe Ser Lys
50 55 60

Leu Pro Met His Asn Ala Ala Tyr Ala Phe Val Lys Asn Arg Ser Ile
65 70 75 80

Lys Ser Asn Ala Leu Leu His Ala Glu Ser Lys Asn Lys Tyr Tyr Val
85 90 95

Lys Ile Asp Leu Lys Asp Phe Phe Pro Ser Ile Lys Phe Thr Asp Phe
100 105 110

Glu Tyr Ala Phe Thr Arg Tyr Arg Asp Arg 1-
115 120

Tyr Asp Lys Glu Leu Leu Gln Leu Ile Lys Thr Ile Thr Glu
130 135 140

Asp Ser Thr Leu Pro Ile Gly Phe Pro Thr Ser Pro Leu Ile Ser
145 150 155

Phe Val Ala Arg Glu Leu Asp Glu Lys Leu Thr Gln Lys Leu Asn
165 170 175

Ile Asp Lys Leu Asn Ala Thr Tyr Thr Arg Tyr Ala Asp Asp Ile Ile
180 185 190

Val Ser Thr Asn Met Lys Gly Ala Ser Lys Leu Ile Leu Asp Cys Phe
195 200 205

Lys Arg Thr Met Lys Glu Ile Gly Pro Asp Phe Lys Ile Asn Ile Lys
210 215 220

Lys Phe Lys Ile Cys Ser Ala Ser Gly Gly Ser Ile Val Val Thr Gly
225 230 235 240

Leu Lys Val Cys His Asp Phe His Ile Thr Leu His Arg Ser Met Lys
245 250 255

Asp Lys Ile Arg Leu His Leu Ser Leu Leu Ser Lys Gly Ile Leu Lys
260 265 270

Asp Glu Asp His Asn Lys Leu Ser Gly Tyr Ile Ala Tyr Ala Lys Asp
275 280 285

Ile Asp Pro His Phe Tyr Thr Lys Leu Asn Arg Lys Tyr Phe Gln Glu
290 295 300

Ile Lys Trp Ile Gln Asn Leu His Asn Lys Val Glu
305 310 315

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1602 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 548..1507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGGCATCTAT TAAGAAGGTT AGGAAAGAAA ATAAAGTATC AAAAGATATT GGAAATATAT 60
TATACGCAGA GCGTTTCTAT TGCCTTGTAT CTATTTACTG GATAGTGTCA ACTACCGCAC 120

ACTGTGTGAA CTAGCTTTTA AAGCGATAAA GCAAGATGAT GTT
 TAGATCCGTT GTTCTCGTC TAATAAATGA ACGAAAAATA CTTCAA
 TCAGGTCCT GCTTTGGGGG CTAGCTATGT TAGGAGCGTC TTTGATAGAA
 CCGATTGCGG CTTGAGATTA TGAATTTTGA AAACCGTAGA AAATCAACAT TTA
 TAAGATTCCG TATGCGCACC CTTAGCGAGA GGTTCATCAT TAAGGTCAAC CTCTGGAA
 TGTTCGGCA TCCTGCATTG AATCTGAGTT ACTGTCTGTT TTCCTTGTTG GAACGGAGAG
 CATCGCCTGA TGCTCTCCGA GCCAACCAGG AAACCCGTTT TTTCTGACGT AAGGGTGCGC
 AACTTTC ATG AAA TCC GCT GAA TAT TTG AAC ACT TTT AGA TTG AGA AAT
 Met Lys Ser Ala Glu Tyr Leu Asn Thr Phe Arg Leu Arg Asn
 1 5 10 180
 CTC GGC CTA CCT GTC ATG AAC AAT TTG CAT GAC ATG TCT AAG GCG ACT
 Leu Gly Leu Pro Val Met Asn Asn Leu His Asp Met Ser Lys Ala Thr
 15 20 25 30 367
 CGC ATA TCT GTT GAA ACA CTT CGG TTG TTA ATC TAT ACA GCT GAT TTT
 Arg Ile Ser Val Glu Thr Leu Arg Leu Leu Ile Tyr Thr Ala Asp Phe
 35 40 45 685
 CGC TAT AGG ATC TAC ACT GTA GAA AAG AAA GGC CCA GAG AAG AGA ATG
 Arg Tyr Arg Ile Tyr Thr Val Glu Lys Lys Gly Pro Glu Lys Arg Met
 50 55 60 733
 AGA ACC ATT TAC CAA CCT TCT CGA GAA CTT AAA GCC TTA CAA GGA TGG
 Arg Thr Ile Tyr Gln Pro Ser Arg Glu Leu Lys Ala Leu Gln Gly Trp
 65 70 75 781
 GTT CTA CGT AAC ATT TTA GAT AAA CTG TCG TCA TCT CCT TTT TCT ATT
 Val Leu Arg Asn Ile Leu Asp Lys Leu Ser Ser Ser Pro Phe Ser Ile
 80 85 90 829
 GGA TTT GAA AAG CAC CAA TCT ATT TTG AAT AAT GCT ACC CCG CAT ATT
 Gly Phe Glu Lys His Gln Ser Ile Leu Asn Asn Ala Thr Pro His Ile
 95 100 105 877
 GGG GCA AAC TTT ATA CTG AAT ATT GAT TTG GAG GAT TTT TTC CCA AGT
 Gly Ala Asn Phe Ile Leu Asn Ile Asp Leu Glu Asp Phe Phe Pro Ser
 115 120 125 925
 TTA ACT GCT AAC AAA GTT TTT GGA GTG TTC CAT TCT CTT GGT TAT AAT
 Leu Thr Ala Asn Lys Val Phe Gly Val Phe His Ser Leu Gly Tyr Asn
 130 135 140 973
 CGA CTA ATA TCT TCA GTT TTG ACA AAA ATA TGT TGT TAT AAA AAT CTG
 Arg Leu Ile Ser Ser Val Leu Thr Lys Ile Cys Cys Tyr Lys Asn Leu
 145 150 155 1021
 CTA CCA CAA GGT GCT CCA TCA TCA CCT AAA TTA GCT AAT CTA ATA TGT
 Leu Pro Gln Gly Ala Pro Ser Ser Pro Lys Leu Ala Asn Leu Ile Cys
 160 165 170 1069
 TCT AAA CTT GAT TAT CGT ATT CAG GGT TAT GCA GGT AGT CGG GGC TTG
 Ser Lys Leu Asp Tyr Arg Ile Gln Gly Tyr Ala Gly Ser Arg Gly Leu
 175 180 185 1117

ATA TAT ACG AGA TAT GCC GAT GAT CTC ACC TTA TCT GCA CAG 1165
 Ile Tyr Thr Arg Tyr Ala Asp Asp Leu Thr Leu Ser Ala Gln Ser 205
 195 200
 AAA AAG GTT GTT AAA GCA CGT GAT TTT TTA TTT TCT ATA ATC CCA A 1213
 Lys Lys Val Val Lys Ala Arg Asp Phe Leu Phe Ser Ile Ile Pro Ser 220
 210 215
 GAA GGA TTG GTT ATT AAC TCA AAA AAA ACT TGT ATT AGT GGG CCT CGT 261
 Glu Gly Leu Val Ile Asn Ser Lys Lys Thr Cys Ile Ser Gly Pro Arg 235
 225 230
 AGT CAG AGG AAA GTT ACA GGT TTA GTT ATT TCA CAA GAG AAA GTT GGG 1309
 Ser Gln Arg Lys Val Thr Gly Leu Val Ile Ser Gln Glu Lys Val Gly 250
 240 245
 ATA GGT AGA GAA AAA TAT AAA GAA ATT AGA GCA AAG ATA CAT CAT ATA 1357
 Ile Gly Arg Glu Lys Tyr Lys Glu Ile Arg Ala Lys Ile His His Ile 270
 255 260 265
 TTT TGC GGT AAG TCT TCT GAG ATA GAA CAC GTT AGG GGA TGG TTG TCA 1405
 Phe Cys Gly Lys Ser Ser Glu Ile Glu His Val Arg Gly Trp Leu Ser 285
 275 280
 TTT ATT TTA AGT GTG GAT TCA AAA AGC CAT AGG AGA TTA ATA ACT TAT 1453
 Phe Ile Leu Ser Val Asp Ser Lys Ser His Arg Arg Leu Ile Thr Tyr 300
 290 295
 ATT AGC AAA TTA GAA AAA AAA TAT GGA AAG AAC CCT TTA AAT AAA GCG 1501
 Ile Ser Lys Leu Glu Lys Lys Tyr Gly Lys Asn Pro Leu Asn Lys Ala 315
 305 310
 AAG ACC TAATGGTCTT CGTTTAAAA CTAAAGCTCA TAGGTTGAAA AATTGAGCAC 1557
 Lys Thr 320
 TTCTTCGTCC AACCAGTTAT TTAGTTCCTG CAATCGTTTC TGCAG 1602

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met Lys Ser Ala Glu Tyr Leu Asn Thr Phe Arg Leu Arg Asn Leu Gly 15
 1 5 10
 Leu Pro Val Met Asn Asn Leu His Asp Met Ser Lys Ala Thr Arg Ile 30
 20 25 30
 Ser Val Glu Thr Leu Arg Leu Leu Ile Tyr Thr Ala Asp Phe Arg Tyr 45
 35 40 45

Arg Ile Tyr Thr Val Glu Lys Lys Gly Pro Glu Lys Arg Met Arg Thr
 50 55 60
 Ile Tyr Gln Pro Ser Arg Glu Leu Lys Ala Leu Gln Gly Trp Val Leu
 65 70 75 80
 Arg Asn Ile Leu Asp Lys Leu Ser Ser Ser Pro Phe Ser Ile Gly Phe
 85 90 95
 Glu Lys His Gln Ser Ile Leu Asn Asn Ala Thr Pro His Ile Gly Ala
 100 105 110
 Asn Phe Ile Leu Asn Ile Asp Leu Glu Asp Phe Phe Pro Ser Leu Thr
 115 120 125
 Ala Asn Lys Val Phe Gly Val Phe His Ser Leu Gly Tyr Asn Arg Leu
 130 135 140
 Ile Ser Ser Val Leu Thr Lys Ile Cys Cys Tyr Lys Asn Leu Leu Pro
 145 150 155 160
 Gln Gly Ala Pro Ser Ser Pro Lys Leu Ala Asn Leu Ile Cys Ser Lys
 165 170 175
 Leu Asp Tyr Arg Ile Gln Gly Tyr Ala Gly Ser Arg Gly Leu Ile Tyr
 180 185 190
 Thr Arg Tyr Ala Asp Asp Leu Thr Leu Ser Ala Gln Ser Met Lys Lys
 195 200 205
 Val Val Lys Ala Arg Asp Phe Leu Phe Ser Ile Ile Pro Ser Glu Gly
 210 215 220
 Leu Val Ile Asn Ser Lys Lys Thr Cys Ile Ser Gly Pro Arg Ser Gln
 225 230 235 240
 Arg Lys Val Thr Gly Leu Val Ile Ser Gln Glu Lys Val Gly Ile Gly
 245 250 255
 Arg Glu Lys Tyr Lys Glu Ile Arg Ala Lys Ile His His Ile Phe Cys
 260 265 270
 Gly Lys Ser Ser Glu Ile Glu His Val Arg Gly Trp Leu Ser Phe Ile
 275 280 285
 Leu Ser Val Asp Ser Lys Ser His Arg Arg Leu Ile Thr Tyr Ile Ser
 290 295 300
 Lys Leu Glu Lys Lys Tyr Gly Lys Asn Pro Leu Asn Lys Ala Lys Thr
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 396..1352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TCACCCTGAA AGACCTGATT GCTTACCTGG AAGAGAAGCC GGAAATGGCG GAACATCTGG	60
CGGCGGTTAA GGCCTATCGC GAAGAGTTCG GCGTTTAAAA ATATGCGCTG TGCAGGGTTT	120
TTGCTGTGCG CAGCGTGATG CGCTTCAAGA TATCGTGTTA ATCTGCTTTC GCCAGCAGTG	180
GCAATAGCGT TTCCGGCCTT TTGTGCCGGG AGGGTCGGCG AGTCGCTGAC TTAACGCCAG	240
TAGTATGTCC ATATACCCAA AGTCGCTTCA TTGTACCTGA GTACGCTTCG CGTACGTCGC	300
GCTGACGCGC TCAGTACAGT TACGCGCCTT CGGGATGGTT TAATGGTATT GCCGCTGTTG	360
GCGCCTCTTT TGGCCGCCGT GATGTGGAGA GTGGA ATG GAT GCT ACC CGG ACA	413
Met Asp Ala Thr Arg Thr	
1 5	
ACC CTT CTG GCG CTC GAT TTG TTC GGC TCG CCG GGC TGG AGC GCC GAT	461
Thr Leu Leu Ala Leu Asp Leu Phe Gly Ser Pro Gly Trp Ser Ala Asp	
10 15 20	
AAA GAA ATA CAG CGA CTG CAT GCG CTC AGT AAT CAT GCC GGA CGC CAT	509
Lys Glu Ile Gln Arg Leu His Ala Leu Ser Asn His Ala Gly Arg His	
25 30 35	
TAC CGA CGC ATT ATT CTT TCT AAA CGC CAC GGT GGT CAG CGG CTG GTG	557
Tyr Arg Arg Ile Ile Leu Ser Lys Arg His Gly Gly Gln Arg Leu Val	
40 45 50	
TTA GCC CCT GAT TAC TTG CTC AAA ACC GTA CAG CGC AAC ATT CTT AAG	605
Leu Ala Pro Asp Tyr Leu Leu Lys Thr Val Gln Arg Asn Ile Leu Lys	
55 60 65 70	
AAC GTC CTT TCA CAA TTT CCG CTT TCC CCT TTT GCT ACA GCC TAC CGA	653
Asn Val Leu Ser Gln Phe Pro Leu Ser Pro Phe Ala Thr Ala Tyr Arg	
75 80 85	
CCA GGT TGC CCA ATC GTC AGC AAC GCG CAG CCA CAC TGC CAA CAG CCG	701
Pro Gly Cys Pro Ile Val Ser Asn Ala Gln Pro His Cys Gln Gln Pro	
90 95 100	
CAG ATC CTG AAA CTC GAT ATC GAA AAC TTT TTC GAT AGC ATT AGC TGG	749
Gln Ile Leu Lys Leu Asp Ile Glu Asn Phe Phe Asp Ser Ile Ser Trp	
105 110 115	
TTA CAG GTC TGG CGT GTG TTT CGC CAG GCC CAG TTG CCA CGT AAT GTG	797
Leu Gln Val Trp Arg Val Phe Arg Gln Ala Gln Leu Pro Arg Asn Val	
120 125 130	
GTA ACC ATG CTG ACC TGG ATT TGT TGT TAT AAC GAC GCG TTA CCG CAG	845
Val Thr Met Leu Thr Trp Ile Cys Cys Tyr Asn Asp Ala Leu Pro Gln	
135 140 145 150	

GGG GCA CCA ACT TCG CCA GCC ATT TCC AAT CTT GTG ATG CGC CGT TTT	893
Gly Ala Pro Thr Ser Pro Ala Ile Ser Asn Leu Val Met Arg Arg Phe	
155 160 165	
GAT GAA CGC ATA GGG GAA TGG TGT CAG GCT CGG GGA ATT ACC TAC ACC	941
Asp Glu Arg Ile Gly Glu Trp Cys Gln Ala Arg Gly Ile Thr Tyr Thr	
170 175 180	
CGC TAC TGC GAT GAC ATG ACC TTT TCA GGT CAC TTC AAT GCC CGC CAG	989
Arg Tyr Cys Asp Asp Met Thr Phe Ser Gly His Phe Asn Ala Arg Gln	
185 190 195	
GTT AAA AAT AAA GTG TGC GGA TTG TTA GCG GAG CTG GGC CTG AGC CTC	1037
Val Lys Asn Lys Val Cys Gly Leu Leu Ala Glu Leu Gly Leu Ser Leu	
200 205 210	
AAT AAA CGC AAA GGC TGC CTG ATA GCT GCC TGT AAG CGC CAG CAA GTA	1085
Asn Lys Arg Lys Gly Cys Leu Ile Ala Ala Cys Lys Arg Gln Gln Val	
215 220 225 230	
ACC GGG ATT GTT GTT AAT CAC AAG CCA CAG CTT GCC CGT GAA GCG CGC	1133
Thr Gly Ile Val Val Asn His Lys Pro Gln Leu Ala Arg Glu Ala Arg	
235 240 245	
CGG GCG CTG CGT CAG GAG GTG CAT TTG TGC CAA AAA TAT GGC GTT ATT	1181
Arg Ala Leu Arg Gln Glu Val His Leu Cys Gln Lys Tyr Gly Val Ile	
250 255 260	
TCG CAT CTT AGT CAT CGT GGT GAA CTT GAT CCT TCT GGC GAT CTC CAC	1229
Ser His Leu Ser His Arg Gly Glu Leu Asp Pro Ser Gly Asp Leu His	
265 270 275	
GCA CAG GCA ACG GCG TAT CTT TAT GCT TTG CAG GGA AGA ATA AAC TGG	1277
Ala Gln Ala Thr Ala Tyr Leu Tyr Ala Leu Gln Gly Arg Ile Asn Trp	
280 285 290	
TTA TTG CAA ATC AAC CCT GAG GAT GAG GCC TTT CAA CAG GCG AGA GAG	1325
Leu Leu Gln Ile Asn Pro Glu Asp Glu Ala Phe Gln Gln Ala Arg Glu	
295 300 305 310	
AGT GTA AAG CGA ATG CTG GTT GCA TGG TAAGAAAAGC GTCAGGCAGA	1372
Ser Val Lys Arg Met Leu Val Ala Trp	
315	
CGTTTCTGCC TGACCGTTTA GGGGAGAATT ACTGCAACTG CGCGGCAATT AGCGGCCAGC	1432
GGGCGTCAAA ATCATCCGTC GGGCGGTATT TAACTCGCT GCGGACAAAA CGTGACAGCA	1492
TACCTTCACA GAAGGCCAGG ATCTGGCTTG CCAGCAGGGT TTCATCGG	1540

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met Asp Ala Thr Arg Thr Thr Leu Leu Ala Leu Asp Leu Phe Gly Ser
 1 5 10 15
 Pro Gly Trp Ser Ala Asp Lys Glu Ile Gln Arg Leu His Ala Leu Ser
 20 25 30
 Asn His Ala Gly Arg His Tyr Arg Arg Ile Ile Leu Ser Lys Arg His
 35 40 45
 Gly Gly Gln Arg Leu Val Leu Ala Pro Asp Tyr Leu Leu Lys Thr Val
 50 55 60
 Gln Arg Asn Ile Leu Lys Asn Val Leu Ser Gln Phe Pro Leu Ser Pro
 65 70 75 80
 Phe Ala Thr Ala Tyr Arg Pro Gly Cys Pro Ile Val Ser Asn Ala Gln
 85 90 95
 Pro His Cys Gln Gln Pro Gln Ile Leu Lys Leu Asp Ile Glu Asn Phe
 100 105 110
 Phe Asp Ser Ile Ser Trp Leu Gln Val Trp Arg Val Phe Arg Gln Ala
 115 120 125
 Gln Leu Pro Arg Asn Val Val Thr Met Leu Thr Trp Ile Cys Cys Tyr
 130 135 140
 Asn Asp Ala Leu Pro Gln Gly Ala Pro Thr Ser Pro Ala Ile Ser Asn
 145 150 155 160
 Leu Val Met Arg Arg Phe Asp Glu Arg Ile Gly Glu Trp Cys Gln Ala
 165 170 175
 Arg Gly Ile Thr Tyr Thr Arg Tyr Cys Asp Asp Met Thr Phe Ser Gly
 180 185 190
 His Phe Asn Ala Arg Gln Val Lys Asn Lys Val Cys Gly Leu Leu Ala
 195 200 205
 Glu Leu Gly Leu Ser Leu Asn Lys Arg Lys Gly Cys Leu Ile Ala Ala
 210 215 220
 Cys Lys Arg Gln Gln Val Thr Gly Ile Val Val Asn His Lys Pro Gln
 225 230 235 240
 Leu Ala Arg Glu Ala Arg Arg Ala Leu Arg Gln Glu Val His Leu Cys
 245 250 255
 Gln Lys Tyr Gly Val Ile Ser His Leu Ser His Arg Gly Glu Leu Asp
 260 265 270
 Pro Ser Gly Asp Leu His Ala Gln Ala Thr Ala Tyr Leu Tyr Ala Leu
 275 280 285
 Gln Gly Arg Ile Asn Trp Leu Leu Gln Ile Asn Pro Glu Asp Glu Ala
 290 295 300
 Phe Gln Gln Ala Arg Glu Ser Val Lys Arg Met Leu Val Ala Trp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Tyr Xaa Asp Asp
1

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Ser Xaa Xaa Xaa
1

6!
Concluded
(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Xaa Val Thr Gly
1